895640101

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OM nucleic - nucleic search, using sw model Run on:

September 25, 2003, 12:10:38; Search time 2162 Seconds (Without alignments) (Without alignments) (Without alignments)

pitie:
Peffectsore: US-10-049-568-1
Peffectsore: 1 474
Sequence: 1 474
Sequence: 1 474 IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

5777422 Total number of hits satisfying chosen parameters:

2888711 seqs, 20454813386 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Databas

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Pred. No. is the number of results predicted by chance to have a 41: em_htgo_other:*

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. SUMMARIES.

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ALIGNMENTS

	PAT 17-MAR-2001							Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo.		
	Linear							Vertebrata;	: Hominidae:		
	p DRA	48.						Craniata;	Catarrhin		
	474 bp	nt W001145		078				Chordata;	Primates;		
		from Pate		GI:13397		(human)	St	Metazoa;	Sutheria;		
	AX088165	Sequence 1	AX088165	AX088165.1 GI:13397078		Homo sapiens (human)	Homo sapiens	Eukaryota;	Mammalia;	7	Duecker, K.
RESULT 1 AX088165		DEFINITION	z	VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS

New g-protein coupled receptor and dna sequences thereof Patent: WO 0114548-A 1 01-MAR-2001;

TITLE

/Mo_Lype="genomic DBM" CDS 1/Acces="mommed protein product" Acces="mommed protein product" Approtein_Lid="mommed protein product" Approtein_Lid="mommed protein product" Approtein_Lid="mommed protein product pr	OGEN MATCH OGEN MATCH 22.7%; SCORE 439.2; DB 6; Leseth 1191; Best Local Shilarity 96.8%; STEAG 10.0.112.0 MATCHER 439; CORRESTWICH 96.8%; STEAG 13; ITGGLS 2; GGPS 1; MATCHER 439; CORRESTWICH 7000-000-000-000-000-000-000-000-000-00	643 OCCASATENCE ACCASACIONE EN ENTRE CONTRACTOR ACCASACIONE E CONTRACTOR DE CONTRACTOR	15 ACCOUNTS AND ANALOGOUS CONTROLLED CONTROL	Dec. Dec.	NACHOLIS 3 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0337 ANSI-0377 ANSI-
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1786 GTTTTTCCTATGGAAGCAGCATGTTTATAGTGTTCATCAAAGTGCCATAACAACTAACAAGTGAACTAAA 1895
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/translation="WTSGSVPFYILIFGKYFSHGGGODVKCSLGYFPCGNITKCLPQL
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                          "Analism-"Homo saplens"
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                                                             /mol_type-"mRNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Romo sapiens leucine-rich repetr-containing G protein-coupled
Rengeloop ( 1687) mRNA, complete cds.
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Pred. No. 1e-91;
0; Mismatches 13; Indels
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                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Location/Qualifiers
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al Similarity 96.8%;
459; Conservative
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COMMENT

MARPING INFORMATION: IMPROMETED TO COLLIS CLOSS WAS PROVIDED BY Dr. John D. MARPING THE TREATMENT OF COMESTION, Parkington Mixestry, Ps. Louis Reventor, see Parts //Resonance.purell.edu/mer apposition of this Reventor, see Parts //Resonance.purell.edu/mer apposition of this	SOURCE INTURNATIONS. Library was made from the blood of one make didnot, and adertically divergenes, two Month PY Library was made from PY. Inches Dr. Franch M. Catenaes, J. 1. and de Yong, P. 1. (1998) has improved the approach for construction of betractical statisfied, incremented by the construction of betractical statisfied, incremented the construction of the process and statisfied in the from the state of the class of the c	NEIGHDORING SENDENCE INFORMATION: CTD-2005A22; the Clone sequenced to the fight is FRIL-665A18. Actual math of this schoe is at base position 18741-655A4; actual end is at base position 187431 of RRI1-575A4.	Sequence derived from one plasmid subclone, base position 102011 to TEMATURES	/App.*/ / / / / / / / / / / / / / / / / / /	repeal_region /Fig	repact_repion (757_1358) repact_repion (757_1481) repact_repion (757_1481) repact_repion 2577. 13069*11	repeat_replon 2731. 1354 *** repeat_replon 2651. 1354 *** repeat_replon 2651. 1354 *** repeat_replon 2651. 1354 *** repeat_replon 2651. 1351 *** repeat_replon 2651. 1371 *** repeat_replon 2651. 1372 *** repeat_replon 2751. 1371 *** replon 2751. 1371 ** replon 2751. 1371 *** replon 2751. 1371 *	repeat_repton (2000, 148) repeat_repton (208, 148)	repost_region 5/87sm7 repost_region 6/8657. Ppt_fmaily**N_rich* repost_region 6/9657. Ppt_fmaily**	repeat_region (66974) repeat_region (74440) repeat_region (75440) repeat_region (75440) repeat_region (11640) refeat_region (11640)
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(C12M1/21, C12H1.19), (C12P21/05/C12R1119), (C12M1/21)
NOVEI G protein-coupled receptor protein and its DNN. FH Key
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Nortya, T., Tohr. Shintani, Y. and Miyajima, N. and Arachia; Wennindes, Nono.

Nortya, T., Tohr. Shintani, Y. and Miyajima, N. and Arachia, M. and Arachia, Wennindes, M. Tohrachia, M. and Miyajima, N. and M. and M
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Novel G protein-coupled receptor protein and its DNA.
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Pred. No. 1.2e-29;
0; Mismatches 117; Indels
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/mol_type-"genomic DNA"
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Best Local Similarity 67.4%;
Matches 242; Conservative
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| 11115. .1138
| //note="match to EST AI652121 (NID:g4736100) wb47c02.Xl*
| 12295. .12442
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"hote-"match to EST AI375172 (NID:g4175162) tc10b12.x1"
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17004. .17094
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Tricted match to EST AN122078 (NID:91678116) zk93910.rl
                                              /note="match to EST A1683385 (NID:q4893567) tx66e09.x1"
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[7655. 17710
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Anche-'similar to Mus musculus EST BR297224
(RID:956401955)*
                                                                                                                                                                                                                                                                                         /note="similar to Mus musculus EST BB297224
(NID:g16401965)"
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Pred. No. 1.5e-41;
0; Mismatches 5;
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complement(17219. .17220)
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9681. .9926
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15194. .15487
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12735, 12900
/rpt_family-"Alu"
13540, 13819
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/rpt_family="L1"
10225. 'ner"
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12443. .12734
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/rpt_family="Alu"
14177. 14344
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15575. .15853
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9053. .9124
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15130. .15150
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[7610. 18078
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17849. .18074
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9126 0:;
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3746. .9052
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A61895/00, A61837/00, GOLM33/15, GOLM33/56, GOLM33/56//
(G13M1/21, G12R319), (C12P21/02, G12R1.19)
Novel G protein-coupled receptor protein and its DNN. FH Noy
Location/Qualifiers
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1. (Reseal to 1473). Primates; Cotarthini; Reminiae; Econ. 1. (Reseal to 1473). Shitani; "A shitani; "
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NOVEL C protein-coupled receptor protein and 1ts DNA.
BD141175
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Pred. No. 1.2e-29;
0; Mismatches 117; Indels
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Homo sapiens
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PC A61K4
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                          CAAGTIAAAAAAGGAIGAICCIIGCCAAACGIITITITCIITAIAGIAITIECIGAIGCA 189
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250 GGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATAACAGTGCTTTGAACCCA 309
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                                                                                                        Chen, R., Dang, H.T. and Lowitz, K.P. 
Endogenous and non-endogenous versions of human g protein-coupled
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Mammalla, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota, Wetazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
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Arena Pharmaceuticals, Inc. (US)
Location/Qualifiers
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AX148176
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
215 c 214 q 361
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(C12N1/21.C12N1.19).(C12P21/02.C12N1.19)
Novel G protein-coupled receptor protein and its DNA. PH Key
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1393 TATATTACTATGTTCTGTTCCATTCAAAAACOGCCTTGCAGACCACAGAAGTAAGGAAT 1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 CAAGTTAAAAAAGAGATGATCCTTGCCCAACGTTTTTCTTTATAGTATTTACTGATGCA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 TTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAGAATACCA 249
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Bukarota; Butheria; Primates; Catarrhin; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 TATTCAGGGCAATTTTTCTTGGTATTAATTTGGCCGCATTATCATCATAGTTTTTTCC
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Leuchher-ich repet-condining g-protein coupled receptor-8
molecules and uses thereof
Perent: NO 0214489-A. 11 21-PEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'organism='Homo sapiens (human)'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 171.8; DB 6
Pred. No. 1.1e-29;
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/organism-"Homo sapiens"
/mol_type="genomic DNA"
/db.zref="taxon:9606"
a 377 c 351 g 586
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AX385037
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1. .2049
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NOVEL O protein-coupled receptor protein and its DNA. FH Roy
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A61K45/00, A61X48/00, A61P1/00, A61P3/00, A61P9/00, A61P25/28, PC
                                       PRESENT: NO 0204640-A 4 17-72A-2002.
TAKEAR-CHROIGAL INOUFFESS LITD, TAKAO MORIYA,TAKAGBI ITO, YASUBHI SHIRWANI, MGHUTUK HITAJHA
GO Homo saptens (human)
FW NO 0204640-A/A (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TAKEDA CHEMICAL INDUSTRIES LID, TAKEO MORIYA, TAKASHI ITO, YASUSHI
                                                                                                                                                                                                                                                                          FF 06-01-0001 MO 2001JP005878
FF 07-011-2000 P 099-21399.18-DE2-2000 JP 00P 383794 PI PAKED MORPHY, 
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Novel G protein-coupled receptor protein and its DNR
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/mol_type="genomic DNA"
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WO 0204640-A/1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 TAIGGAAGCAICTITTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAAT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1702 TRIBATTACTATGTTCTGTTCCATTCAAAAACCGCCTTGCAGACCACAGAAGTAAGGAAT 1763
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Kallick, D.A., Gondell, A.R., Wallan, N.R., Avriga, C.R. Ellotet, V.S.,
Rafallan, A.J., Randman, J.J., Pall, J., Tang, Y.T., Yoe, H., Raddy, R.,
Benford, M., Lub, D.M., Grafall, R.C., Khang, F.M., Rahba, R.T., 1800, C.H.
Richardson, P. W., Cattfall, J.A., Werren, B.A., Yong, J., Wee, B.A. and
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Mammalla, Butherla, Primates, Cataribla, Hominidae, Homo.
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11 Similarity 67.4%; PredG No. 1.18-29; Le-29; 242; Conservative 0; Mismatches 117; Indels 0; 242; Conservative
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                                                                                                                                                                                                                                       Pred. No. 1.1e-29;
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Patent: WO 02063004-A 49 15-AUG-2002;
Incyte Genomics, Inc. (US)
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AX709190
      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
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TEDIOSKOS SIGJILGATARALAFIYELFNIKDYTSKYYLFELEVNSALNYETYTLTY
                                                                                                                                                                                                                                                               /translation="MIVFLVFKHLFSLRLITMFFLHFIVLINVKDF8170GSMITPS
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Nammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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A norwal human grancett normal resemblishing cs. and sawken D.R.
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Pred. No. 1.1e-29;
0; Mismatches 117; Indels 0;
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/organism="Homo sapiens"
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Search completed: September 25, 2003, 13:58:08 Job time : 2168 secs

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GenCore version 5 1.6 Copyright (c) 1993 - 2063 Compugen Ltd.	OW nuclaic - nuclaic search, using sw model Rum on: Suptember 25, 2003, 12:09:23; Search time 222 Seconds FORD on: Suptember 25, 2003, 12:09:09:09:09:09:09:09:09:09:09:09:09:09:	Title: 8021-049-568-1 4740-149-568-1 5021-049-568-1 746-140-140-140-140-140-140-140-140-140-140	able:	Searched: 2552756 seqs, 1349719017 residues Total number of hits satisfying chosen parameters:	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 03 Maximum Match 1008 Listing first 45 summaries	Database : N_Geneseq_19Jun03:* //SIDSI/Ogdata_Ageneseq/geneseq_0eneseque_embl/NAl980.DAT:* //SIDSI/Ogdata_Ageneseq_oeneseque_embl/NAl981.DAT:*					211. // STIENT /	Pred. No. is the number of results predicted by chance to have a soore greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES Result Query Wo. Score Match Length DB ID	1 479 1000 4.42 Mazgasos 0 1492 2 227 1169 22 Mazgasos 4 499.2 29.7 1159. 22 Maxgasos 5 499.2 29.7 1159. 22 Maxgasos 6 499.2 29.7 1159. 24 Maxgasos 6 499.2 29.7 129. 24 Maxgasos 6 499.2 29.7 2246. 25 Maxgasos 8 499.2 27.7 2246. 25 Maxgasos

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Pred. No. 4.9e-119;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                  Claim 5; Page 35-36; 36pp; English
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Best Local Similarity 100.0%;
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2000US-0231968 2000US-0232397

AAI99557 standard: cDNA: 1089 BP

04-JAN-2002 (first entry)

AA199557; RESULT 2 AAI99557 ID AAI99 XX AC AAI99 XX

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The invention statists to possible ALMSSP45-ALMSSP45 in protecting should be senting the senting of manifolding set and senting or senting the senting senting set and senting Isolated digestive system associated polypeptide for treating, seventing and to prognabing disorders related to the digestive system including digestive system cancers and also for testing and detection Claim 1, SEQ ID NO 20, 509pp + Sequence Listing; English. Ruben SM: 25 - 25 - 2000; 20003- 253198. 65 - 255 - 2000; 20003- 2036719. 69 - 252 - 2000; 20003- 2031479. 69 - 252 - 2000; 20003- 253168. 69 - 252 - 2000; 20003- 253188. 69 - 252 - 2000; 20003- 253189. 69 - 252 - 2000; 20003- 253189. 69 - 252 - 20003- 253189. 65 - 248 - 20003- 253199. 65 - 248 - 20003- 253199. 65 - 248 - 20003- 253199. (HUMA-) HUMAN GENOME SCI INC Rosen CA, Barash SC, WPI: 2001-465573/50 P-PSDB: AAM99945 e.g. diagnosis

Sequence 1089 BP; 386 A; 186 C; 186 G; 331 T; 0 other;

9 61 GITITITICCIAIGGAAGCAIGITITATAGIGITCAICAAAGIGCCAIAACAGCAACIGAA 120 80 GTTTTTCCTATGGARGCATGTTTTATAGTGTTCATCAAGTGCCATAACAGCACTGAA 139 240 241 GABATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT 300 20 GCCCAGATTTATTCAGTGCCAATTTTTCTTGGTATTAATTTGGCCGCATTTATCATA 79 1 GCCCAGATTTATTCAGTGGCAATTTTTCTTGGTATTAATTTGGCCGCATTTATCATCATA 181 ACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACGGTA 260 GNANTACCAGGGGCCATTAACCTGTGGGAGTGATTTTATTATTCTGCCCATTAACAGGTGCT 92.7%; Score 439.2; DB 22; Length 1089; 96.8%; Pred. No. 1.8e-109; dive 0; Mismatches 13; Indels 2; Gaps al Similarity 96.89 Query Match Best Local S1 Matches 459; ð g ŏ a ð 8 ð g à g TTGAACCCAATTCTCTATACTCTGACCACAAAGACCATTTAAAGAAATGATTCATCGTTT 360 320 TYGAACCCAATYCTCTATACTCTGACACAAGACATTAAAGAAATGATCATCGGTTT 379

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30 - Aug - 2000; 01 - SEP - 2000; 01 - SEP - 2000; 01 - SEP - 2000; 01 - SEP - 2000; 05 - SEP - 2000; 05 - SEP - 2000;	06-SEP-2000; 06-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000; 08-SEP-2000;	PR 08-SEP-2000; 2000US-0231414 PR 08-SEP-2000; 2000US-0232080 PR 12-SEP-2000; 2000US-0232968 PR 14-SEP-2000; 2000US-0232968		27 - SEP - 2000; 27 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000; 29 - SEP - 2000;	R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID No 163; 837pp; English.
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food additives or preservatives
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2000US-0250391.
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2000US-0251479
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01-DEC-2000;
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1 GCCCAGNITIATICAGIGGCAATITICIIGGIATIAATITGGCCGCATTAATCATCATA 60 Gaps 5 Indels 0; Mismatches Similarity 96.8 59; Conservative Best Local Sim Matches 459:

Score 439.2; DB 23; Length 1162;

Pred. No. 1.8e-109;

96.8%;

Query Match

(PHAA) PHARMACIA & UPJOHN CO.

99US-0429517. 99US-0429555. 99US-0429676. 99US-0429695.

99US-0454399 2000US-0481794

12-JAN-2000;

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Dyspetities and polymententides encoding them. The polymetication and polymetications are considered to the polymetication sembled proteins are considered to the polymetication of the polymetication and the polymetication of the polymeti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein coupled protein receptor peptides useful for the prevention, diagnosis and treatment of cell proliferative, neurological
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                                                              Human GPCR protein (HGPRP) encoding cDNA (clone ID 2488822).
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                                                                                                                                                                 Seven transmembrane receptor polypeptides and polymuchectides, useful for treating neurological or psychiatric disorders, e.g. rehizophrenia, as well as for identifying compounds useful for treating schizophrenia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1191 BP; 340 A; 229 C; 226 G; 396 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.7%; Score 439.2; DB 22;
96.8%; Pred. No. 1.8e-109;
live 0; Mismatches 13;
                                                                                                                                                                                                                                                                                              Claim 22; Page 15-16; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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Matches 459; Conservative
                               Wood LS,
                                                                                   WPI: 2001-328653/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                             P-PSDB, AAR0249B,
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                                                                                                                                                                                                                                                                                                                                                             61 GTTTTTTCCTAFGGAAGCAFGTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      912 AFACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTAFAGTATTT 971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 ACTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTTCAGGTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 GARATROCREGIRCCAIRACCICTIGGGTRGIGATTGGTTATTCTGCCATTAACAGTGCT 300
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                                                                                                                                                               DB 24; Length 1804;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human G protein-coupled receptor LGR7 nucleotide SEQ ID NO:622.
                                                                                                                                                                                                                                           Indels
                                                                                   Sequence 1804 BP: 563 A: 318 C: 327 G: 596 T; 0 other;
                                                                                                                                                        Score 439.2; DB 24
Pred. No. 2.1e-109;
       encodes a human GPCR protein of the invention.
                                                                                                                                                                                                                                           0; Mismatches
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                                                                                                                                                               92.78;
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                                                                                                                                                                                                     96.88;
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                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                               Query Match
                                                                                                                                                                                                             Local
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AB242570
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The invention cather to an inclusive SQM meading Growin

As included trapect of the DQMs, species writeran maring

at least 73% identity to the GDMS, wector computation has included

at least 73% identity to the GDMS, wector computation that include computation to the Competition Control of Control 
1032 GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTTTTATTCTGCCCATTAACAGTGCT 1091
                                                                                                                         1152 TGGTATAACTACAGACAAAAAAAAAATGTATGGACAGCAAAGG--TCAGAAAACATATGGTC 1209
                                                                                                                                                                                                                                           361 TGGCATAACTACAGACAAAATCTATGGACAGCAAAGGTATCAGAAACATATGCTC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; 88; gene; G-protein coupled receptor; GPCR; neoplastic disorder; neurological disorder; minume disorder; cytostaric painteatic concer; fellicular carcinose of the thyroid; lekomyoma of the uterus; epileps;
                                                                                   TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCATICALCIGGGGGAAAIGIGGCCACIGCAGAGAIGCCACCIGAGITAA 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human G-protein coupled receptor cDNA #4, Incyte clone 2488822CB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      che
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diagnosis, prognosis, treatment and evaluation of therapies for
neoplastic, neurological and immine disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baughn MR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX73054 standard; cDNA; 1804 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-JUN-2001; 2001US-0895686.
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(TANG/) TANG Y T.
(BAUG/) BAUGHN M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandman O, Lal PG,
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us-10-049-568-1.rnq

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The present investion describes antiquate particle (1) competitive response (1) consistent and c
                                                                                                                                                                                                                                                New isolated antigenic peptides e.g., for G protein-coupled receptors (GENE), useful for diagnoshing and destaining drugs for treatment conditions in which GPCEs are involved, e.g. AIDS, Alzheimer's disease, conditions to
                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure: Fig 1: 523pp: English.
(LIPE-) LIPESPAN BIOSCIENCES INC
                                                                           Brown JP;
                                                                                                                                                                                                                                                                                                                                                              cancer or autoimmune diseases
                                                                    Roush CL,
                                                                                                                                         WPI; 2003-046718/04.
                                                                                                                                                                                  P-PSDB; ABP81724
                                                                           Burmer GC,
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loss eligiegy, serkes tuberchoisis, dossity, numena hypertension, prepension, send disorders, tuberchoisis, dossity, numen disorders the thomstoid artifatis, transa, dieres, or any other disorder in which GRORs are irroyaed, services saw ye used in immunossays and immunolaymosis. Andrissa to antichoise saw ye used in immunossays and immunolaymosis. Andrissa to antichoise saw ye exequilities of the present invasition. Seguence 2274 BP; 669 A; 460 C; 421 G; 724 T; 0 other;

New G-protein coupled receptors, useful for identifying their own

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memory

depression, schizophrenia, dementia, mental retardation,

anxiety,

or

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1919 GCCGGGATTTATTCAGTGGCATTTTTTTTTGTTGGTAATTTGGCCGCATTTATCATCATA 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1979 GTTTTTCCTATGGAAGCATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAA 2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GTTTTTCCTATGGAAGCATGTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present resource sectors the hammer of protects coupled response to the buring extraceallust leading for the repeat regions, designated information form. The support of the properties are used to the facility for leading the leading of the support of the polypeptides made on the control of the resource sees the control of the resources, described as to this owner the remains on the things of the resources, sees the resource sees the resource in the resource of the resou
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2467 BP: 747 A: 487 C: 474 G: 759 T: 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The proteins are also expressed in diverse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Fig 3; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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Pred. No. 2.3e-109;
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2, Gaps

DB 20; Length 2467; 13; Indels

2.3e-109;

Score 439.2; Di Pred. No. 2.3e-0; Mismatches

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                                                                                                                                                                                                                                          Human; LGR4; LGR5; LGR7; G-protein coupled receptor; gene therapy; extracellular leucine rich repeat region; mapping; identification;
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                                                                                                                                                                                                          Juman IGR7 long form nucleotide sequence.
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                                                                                                              AAZ25345 standard: cDNA: 2467 BP
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Length 3584;
                                                                                                             2,
                                                                                                   Indels
DB 20;
Score 439.2; DB 20;
Pred. No. 2.6e-109;
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04-PER-2000; 2000US-0180CSB.

12-PER-2000; 2000US-0184564.

12-PER-2000; 2000US-0186530.

117-PER-2000; 2000US-018937.

117-PER-2000; 2000US-0189123.

118-PER-2000; 2000US-0189123.
92.74;
ilarity 96.8%;
Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                   Human; LGR4; LGR5; LGR7; G-protein coupled receptor; gene therapy;
extracellular leucine rich repeat region; mapping; identification; ss.
                                                                                                                                                                                                                 241 GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3584 BP; 1124 A; 670 C; 647 G; 1139 T; 4 other;
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(ORGA ) ORGANON NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ25346 standard; cDNA; 3584 BP
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2000US-250391P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -NOV-2000;
-DEC-2000;
-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-2000;
                                                                                                                                                                                                                   Human; gene therapy; neural disorder; immune system disorder;
muscular disorder; reproductive disorder; gastrointestinal disorder;
pulmonary disorder; cardiovascular disorder; renal disorder;
proliferative disorder; hillammation; ss.
ABA06471 standard: cDNA: 530 RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.778-2000 200009 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110.000 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001; 2001WO-US01349
                                                                                                              (first entry)
                                                                                                                                                                   Human CDMA SBC ID NO: 137
                                                                                                                                                                                                                                                                                                                                                                                                                W0200154474-B2
                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                              10-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-AUG-2001
                                                          ABA06471;
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CDNA encoding for human uterine motility-association polypeptide #15.
                                                                                                       Human; uterine motility-association disorder; uterus; pregnancy;
labour; menstrual cycle; gene therapy; ss.
                                                                                                                                                                                                                                                              11. **Ab. 2000; 200009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009; 010009
                                                                                                                                                                                                                                       17-JAN-2001; 2001WO-US01317
                                             (first entry)
                                                                                                                                                                              NO200155201-A1
                                                                                                                                                    dono sapiens.
                                             21-NOV-2001
                                                                                                                                                                                                              02-AUG-2001
                 AS28950:
     The present invention provides human cDNAs, proteins and related genomic observables be used in the treatment of neutral, laterage special neutral prescudentive, estrohitekethal, pulbocary, cardiovasoular, and and popilizative discretives and inflammation. The present sequence is a cDNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 GITTITICCIATGGAAGCAIGITTATAGAGTCAACAACAGCCATAACAGCAACTGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 GTTTTTCCRIGGAAGCAIGTTTATACAGTGTTCARCAAGTGCCATAACAGCAACTGAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 ACTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GAAATACCAGGTACCATAACCTCTTGGGTAGTGGTTATTGTTGTTGTTAACAGTGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGAACCCAATTCTCTATACTCTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTT 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GCCCAGATTTATTCAGTGGCAATTTTTCTTGGTATTTTGGCCGCATTTATCATA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecule encoding an inflammation-associated polyperide is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Querr Watch 92.6%; Score 438.8; DB 22; Length 530; Best Local Similarity 96.6%; Pred, No. 1.5e.109. Maker Bard 158; Conservative 1; Mismatches 13; Indels 2; Matches 458; Conservative 1; Mismatches 13; Indels 2;
                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO: 137; 859pp + Sequence Listing; English:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 530 BP; 158 A; 105 C; 95 G; 171 T; 1 other;
                                                                                                                                                                                                           Rosen CA, Barash SC, Ruben SK,
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           (HUMA-) HUMAN GENOME SCI INC
2000HS-251030P
                                                                                                                                                                                                                                       WPI; 2001-476161/51.
P-PSDB; ABB10249.
05-DEC-2000;
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20000S-0249211.
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2000US-0249213.
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2000US-0249218.
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2000US-0256719
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117-W
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17-NOY-2000; 2
01-DEC-2000; 2
01-DEC-2000; 2
05-DEC-2000; 2
05-DEC-2000; 2
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181 ACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention states to the inclusion of cover hamon retrain entities seasons to state the state of the sequences of other price of the state of the stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITTITICCTATGGAAGCAIGTTTATAGTGTTCATCAAAGTGGCATAACAGCAACTGAA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTTTCCTAINGAAGCAIGTTTTATATATGTTCTATCAAAGTGCCATAACACCAACTGAA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.1 ATACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIGANCCCANTICICIATACICISACCACAAGACCATITAAAGAAATGATICATGGTTT 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGCATAACTACAGACAAAGAAAATCTSTGGACAGCAAAGGTATCAGAAAACATATGCTC 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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therewhing and/or promoting disolates related to uterine mobility 
of disolated second with pregnancy and the menatural cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 530 BP; 158 A; 105 C; 95 G; 171 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published pct sequences
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20000S-0251479,
2000US-0251856,
2000US-0251869,
2000US-0251869,
2000US-0251990,
2000US-0251990,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rosen CA, Barash SC, Ruben
                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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Conservative
                                                                                                                                                                                                                                                                                          2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-488777/53.
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Matches 458; Conserv
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06-DBC-2000;
08-DBC-2000;
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Onery Match Barlanity 95.64; Scree 418.8; DB 22; Length 530; Barst Local Similarity 96.64; Pred: No.11.96-1199; Indels 2; Gaps Watches 459; Conservative I; Mismatches 13; Indels 2; Gaps	1. GCCCAGAITTATTCAGIGGCAATTTTCTTGGIATTAATTTGGCCGCATTATCATA	2 GCCCAGALTTATTCAGTGGCAATTTTTCTTGGTATTAATTTGGCCGCATTTATCATCATA	61 GTTTTTCCTATGGAGCATGTTTATAGTGTTCATCAAGTGCCATAACAGCAAGTGAA	62 GTTTTTCCTATGGAAGCATGTTTATAGTGTTCATCAAAGTGCCATAACAGCAGAA		2 ATACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACGTTTTTTTT	1 ACTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTTCAGCTA		GAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTG	2 GAANINCCAGGIACCAIDACCICITGGGIAGIGAITITATICTGCCCATTACAGTGCC		2 TIGAACCCAAITCICIAIACICIGACCACAAGACCATITAAAGAAAGAATCATCATCAGGITT	1 TGCCATAACTACAGAAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTC	- 64	1 CATCATTCATCTGGGGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGTAA 474	O CATCATTCATCTGGGTGGAAATGTGGCCACTGCAGGGGAGATGCCACCTGAGTAA 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCCAGATTTATTCAGTGGCAATTTTTCTTGGTAATTTGGCCGCATTTATCATCATA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 439.2; DB 14; Length 1089;
Pred. No. 7.8e-111;
0; Mismatches 13; Indels 2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Rosen et al. TILLS OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE SPERSNOE: P720301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prior Application removed - See file Wrapper or Palm NUMSER OF 80D IN NOS: 116
SEQ ID NOS: 120
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LENGER: Percents Ver. 2.0
                                                                                                                                                US-09-965-536A-1
US-09-928-175-1
US-10-229-735-2
US-10-222-668-1
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US-09-928-175-19
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CURRENT FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 20, Application US/10073885
Publication No. US20030096346A1
GENERAL INFORMATION:
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Matches 459; Conservative
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Sequence 10, Appl
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Sequence 131, Appl
                                                                                                                                                                   September 25, 2003, 13:56:14 ; Search time 190 Seconds (Without alignments) (Seconds 6216,655 Million cell updates/sec
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                        GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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APPLICANT: THE TWOM, ORDER DE.

APPLICANT: SHIRTON, CHENING.
THE OF THE OFFICE STATES AND ANTHODIES FOR G PROTEIN-COPIED RECENT PRIZE SEPRENCE: 1504-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4, 2004-4
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                                                   1210 CATCATTCATCTGGGTGGAAATCTGGCCACTGCAGGAGGAAGCCACCTGAGTTAA 1263
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        421 CATCATTCATCTGGGGGGAAATGTGGCCACTGCAGGAGATGCCACCTGAGTTAA 474
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Pred. No. 1.2e-110;
0; Mismatches 13; Indels 2;
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APPLICART: Rosen et al.
THIS OF LINEARION: Nucleic Acids, Proteins, and Antibodies
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILTING DAFE: 2006-12-19
                                                                                                                                                                                                                                                                                                               Sequence 622, Application US/10225567A Publication No. US20030113798A1 GENERAL INFORMATION:
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Patent No. US20020090672A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LifeSpan Blosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glenna C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 622
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Best Local Similarity 96.8%;
Matches 459; Conservative
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US-10-225-567A-622
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241 GAMATACCAGGTACCATAACCTCTTGGGTAGTGATTGGGTTATTCTGCCATTAACAGTGCT 300
                                                   301 TIGAACOCAATICICIATACICIGACCACAAGAGACCATITAAAGAATGATTCATCGGTTT 360
                                                                                                                                                                                                                                 320 TEGRACOCRATECTORARACTOTICALITATION TO TEGRACOCRATIVARAGARANGATOSTOSTITE 379
                                                                                                                                                                                                                                                                                                                                                          TGGCATAACTACAGAAAGAAAATCTATGGACAGGAAAGGTATCAGAAAACATATGCTC 420
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O THE INFORMATION: Incyte ID No. US20020106655A1 2488822CB1
US-09-885-10
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96.8%; Pred. No. 1e-110;
1ve 0; Mismatches 13; )
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US-09-895-686-10
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GREERL N. 552570.

FREERL NROBATION:

TILE OF INTREPARED N. K., Saffer, J.D.,

TILE OF INTREPARED N. S. Ashinosila Sequence, Methods Of Detection

TILE OF INTREPARED OF A Malmosila Sequence, And Nethods Of Detection of Salmonalla

TITE OF INTREPARED OF A MANDROM OF A
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                                                                                                                           7124 AARTIGOCATBARARGAGATGAAAAAAGTATITAGTATAAAAAATCTIGTICATCGATA 7065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 AAAGIGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAAGAGATGATCCTTGCCA 157
                                                                           98 AANGIGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAAGAGATGATCCTTGCCA 157
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                            0; Gaps
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TITLE OF INVESTION: A Salmonalla Sequence, Mathods Of Detection
TITLE OF INVESTION: Of A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.1%; Score 38.4; DB 2; Leugth 8967; Peet Incol. Sanitarity 38.5%; Pred. No. 0.53; Analogo Natches 37; Conservative 23; Mismarches 36; Indels 0;
    Best Local Similarity 62.5%; Pred. No. 0.53;
Matches 60; Conservative 0; Mismatches 36; Indels
                                                                                                                                                                                                      1064 AAGAGTTTTTTATATGATATTTTTACTCTTATACTAT 7029
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MEDIUM TYPE: Diskette 3.50", 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
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ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
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FILING DATE: Unknown
                                                                                                                                                                                                                                                                                                                                                Sequence 67, Application US/08853659A
Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/08853659A; Patent No. 5925522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Paul W. Zimmerman
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FILING DATE: n/a
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LENGTH: 8967 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEC ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SECURIORS: 67
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Washington
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US-08-853-659A-67
                                                                                                                                                                                                                                                                                                RESULT 6
US-08-853-659A-67
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TITURE OF INTERNION: A Salmonella Sequence, Nethods Of Detection
TITURE OF INVESTION: Of A Salmonella Sequence, And Methods Of Detection Of Salmonella
TITURE OF INVESTION: Salmonella Sequence, And Methods of Detection Of Salmonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AACGITITITICITIAIAGIATITACIGAIGGAITAI 193
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MEDIUM TYPE: Diskette 3,50", 1,44 Mb storage
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OPERATING SYSTEM: MS-TOS
SOFTWARE: Nord Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
                                                                                SOFTWARE: Word Processor (WordPerfect 5.1) CURRENT APPLICATION DATA:
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ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PNNL P.O. Box 999
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FILING DATE: Unknown
                                                                                                                               APPLICATION NUMBER: US/08/853,659A
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                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSE: Paul W. Zimmerman
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                                                                                                                                                  FILING DATE: UDKNOWN CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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FILING DATE: n/a
                                                             OPERATING SYSTEM: MS-DOS
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LENGIH: 8967 bases
                                 COMPUTER: IBM PC/XT/AT
                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 8967 bases
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STATE: Washington
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                           TYPE: nucleotide
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                                                                                                                                                                                                                                                      FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                   Query Match
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TITLE OF INVENTION: Salmonella Sequence, And Methods Of Detection Of Salmonella NUMBER OF SEQUENCES: 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPICOMET NOON, K. K., Saffer, J.D.
TITLE OF INVENTION: A Salmonella Sequence, Methods of Detection
TITLE OF INVENTION: Salmonella Sequence, And Wethods of Detection of Salmonella
TITLE OF INVENTION: Salmonella Sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22858 AARTIGCCATAAAAACAGAIGAAAAAAAGIATITAGIATAAAAAAICTIGTICATCGATA 22799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Omery Match 8.1%; Score 38.4; DB 2; Length 24701; Best Local Saillarity 62.5%; Pred. No. 0.68; AMAtches 60; Conservative 0; Mishmatches 36; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 AACGITTITCITTATAGTATTIACTGATGCATTAT 193
                                                                                                                                                                                                                                                                          COMPUTER REALIZED FORM:
MEDIUM TYPE: Diskette 3.50", 1.44 Nb storage COMFUTER: IBM PC/XT/AT
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                                                                                                                                                                                                                                                                                                                                                                   SOFTWARES NOT PROCESSOR (WordPerfect 5.1)
CHREMEN APPLICATION NATH, WORDSER: 05/08/853,659A
FILLING DATE: UNLOAM
CLASSITICATION: 435
PATOR APPLICATION 435
PATOR APPLICATION ANS.
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SOFTWARE: Word Processor (WordPerfect 5.1)
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                                                                  AUDRESSEE: Paul W. Zimmerman
AUDRESSEE: Faul W. Zimmerman
AUDRESSEE: Datelle Medocial Institute
AUDRESSEE: Paul D. Dox 999
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TYPE: nucleotide
STRANDEDNESS: double stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 3, Application US/08853659A
; Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: n/a
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                     MS-DOS
                                                                                                                                                           STREET: Washington Way
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CITY: Richland
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CORRESPONDENCE ADDRESS:
                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                Washington
: U.S.A.
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US-08-853-659A-3
                                                                                                                                                                                                                                  COUNTRY:
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APPLICADE: NEASH, F.K.f. Saffer, J.D.
THILD GE IMPRESSION: A Salamonila Sequence, Methods Of Detection
THILD OF THRESTON: Of A Labouella Sequence, And Methods Of Detection
THILD OF THRESTON: Salamonila Sequence, and Methods Of Detection Of Salamonila
NUMBRR OF SEQUENCES: 67
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                                                                                                                                                                                                                                                                                                                                            98 AAASTGCCATAACAGCAACTGAAATACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCA 157
                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36; Indels 0; Gaps
                                                                                                                                                                                                                               / Match Bills: Score 38.4; DB 2; Length 24/01; Local Similarity 61.8; Pred, No. 0.68; Indels 0; conservative 0; Mismatches 35; Indels 0; des 60; Conservative 0; Mismatches 35; Indels 0;
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8.18; Score 38.4; DB 2; Leagth 24701;
Best Local Similarity 62.59; Pred. NO. 0.68; D. Nismatches

9; Manches 69; Conservative 0; Mismatches 36; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                               158 AACGTTTTTCTTATAGTATTTACTGATGCATTAT 193
1904 AAGAGTTTTTTATGATATTTTTACTGATACTAT 1939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: MS-DOS
SOFTWARE: Nord Processor (WordPerfect 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Paul W. Zimmerman
ADDRESSEE: Battelle Memorial Institute
ADDRESSEE: PWNL P.O. BOX 999
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; Sequence 60, Application US/08853659A
; Patent No. 5925522
                                                                                                                       STRANDEDNESS: double stranded
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               INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: none
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskett
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US-08-853-659A-60
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### documentative 1; Wismatches 11; Indeis 2; caps 0 cccodartarizations 0 cccodartariza	0 1 1 1 1 1 1 1 1 1	RESULT. RES	Query Watch Park
PRIOR APPLICATION NUMBERS: 607/41,808 PRIOR APPLICATION NUMBERS: 607/41,806 PRIOR PARTICATION MARKERS: 607/41,806 PRIOR PRIOR PRINCE CALL SECTION OF SECTI	0 0 0 0 0 0 0 0 0 0	09 24 OAN-DAN-DAN-DAN-DAN-DAN-DAN-DAN-DAN-DAN-D	Sequence in Application 02/09/64886 CHARLOW THE PRODOCTION 02/09/64886 CHARLOW THO PRODOCTION 02/09/64886 CHARLOW THO PRODOCTION 02/09/64/886/ THE OFF THE OFF THOSE MICH AND 02/09/14/886 PROGRAM THE OFF THOSE MICH AND 02/09/14/886 PROGRAM THE OFF THOSE MICH OFF THOSE MICH OFF THOSE MICH OFF THOSE OF

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92.3%; Score 437.6; DB 4; Length 1126;

Best Local Similarity 96.6%; Pred. No. 3.55-106;

Matchise 458; Conservative 0; Mismatches 14; Indels 2;
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O'THER INPORMATION: Incyte ID No. 6492505 3556218CT1
IG-0-495-050A-255
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US-09-657-474-7
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ORGANISM: Homo sapiens
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core greater than or equal to the access of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 79,
Sequence 79,
Sequence 3, Al
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Search Jerentz, 8,14; **

Search Jerentz, 8,14; **

Search S, Frodtz, 7/1,10x/6, COMB. seq; **

Sept. Frodtz, 7/1,10x/6, COMB. seq; **

Sept
                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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a	414 FIGAACCCAATCTCTAFACTCTGACCAAGCAFTTAAAGAAATCATCACTGTTCA 473	; GENERAL INFORMATION: ; APPLICANT: Wong, K.K.;
& a	361 IGGONTANCIACANCANGANANCIANGGACONGCIANGGIPATCAGANANCHYC 420	TITLE OF INVENTION: A S. TITLE OF INVENTION: Of . TITLE OF SEQUENCES: 67
oy.	431 OATOATTOATTOATTOATTOATTOATTOATTOATTOATT	CORRESPONDENCE ADDRESS: ADDRESSEE Faul W. Zi. ADDRESSEE Intellecture ADDRESSEE Battelle W. ADDRESSEE PATER P. D.
RESULT US-08-8 ; Seque ; Paten	3807.75-65938/C. Segenance 25.95[Lotton US/0883559A. Riemt No. 593532	STREET: Washington Wa CITY: Richland STATE: Washington COUNTRY: U.S.A.
	RIRRALITENDRALITON: TITEL OF INVENTION: A. K., Saffer, J.D. TITEL OF INVENTION: O. Salmonella Sequence, Methods Of Detection	COMPUTER READABLE FORM: COMPUTER: IBM PC/NT/AN COMPUTER: IBM PC/NT/AN COMPUTER: LAW PC/NT/AN COMPUTER: LAW COMPUTER: MC-I
	TITIES THYRATION: SAlmonella Sequence, And Methods Of Detection Of Salmonella Mindage OF SUCHRENCES: 67 CORRESPONDENCE ADDRESS:	
	ADDRESSE: Paul W. Zimmerman ADDRESSE: Intellectual Property Services ADDRESSE: Battelle Memorial Institute	FILING DATE: Unknown ; CLASSIFICATION: 435 ; PRIOR APPLICATION DATA:
	ADDRESSEE: PNRI, P.O. Box 999 STREET: Weshington Nay CITE: Richland	; APPLICATION NUMBER: D. FILLING DATE: D/A : INFORMATION FOR SEC ID NO:
	STATE: Washington COUNTRY: U.S.A. TTD. 00347 U.S.A.	SEQUENCE CHARACTERISTICS ILENGTH: 8967 bases
	協会を	; STRANDEDNESS: double ; TOPOLOGY: linear
	COMPANIES INCOME WAS NOT OPERATING SYSTEM: MS-DOS SOFTWARE: Word Processor (WordPerfect 5.1)	OTHER INFORMATION: SE OTHER INFORMATION: nu
	APPLICATION UNDER: US/08/853,659A	9-4
	FALLOW DAILS: UNKINGWI CLASSIFICATION: 435 PRIOR APPLICATION DATA:	Query Match Best Local Similarity 62. Matches 60; Conservative
		98 AAA
A 	IMPORMATION FOR SEG ID NO: 28: SEGUENCE CHARACTERIZICS: TENTH: 1107 heads	Db 7124 AAATTGCCATAAAA
	TTPR: notlectide TRANSDURGS: double stranded moderace. linear	Oy 158 AACGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
	PREFITE: OTHER THYPOMATION: the coding nucleotides of SED ID OTHER THYPOMATION: No.12 GOOTEspond to nucleotides 22530 through OTHER THYPOMATION: 24476 of SED ID No.2	SULT 4 -08-853-659#
Out Beg	Oueve substants Oueve Substants (8.1%; Score 38.4; DB 2; Length 1197; Beet Local Salinative G.18; Pred. Abo. 656; Matches 60; Conservative 0; Minanciches 36; Indels 0; Ospo 0;	sequence 9, Application US/ ; Patent No. 592552 ; GENERAL INFORMATION: ; APPLICANF: WORG, K.K.; ; ; TITLE OF INVENTION: A S.
8 8	98 AANGROCKENACHGGAACHGAATRAACHAAAAAAAAAAAATROCK 157 	
δō	158 AACCITTITCITIALAGRATTHCTGATGCATAT 193	ADDRESSEE: Paul W. Zi.
셤	169 AAGAGTITTTARGATTTTTAGCGTARAGATAT 134	ADDRESSEE: Battelle M ; ADDRESSEE: PNNL P.O. I ; STREET: Washington War
RESULT 3 US-08-85 ; Sequen ; Patent	The Section 5 of Section 1970 (1985) Section 1	COMPUTER READABLE FORM:
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Saffer, J.D.
Salmonella Sequence, Methods Of Detection
Ralmonella Sequence, And Methods Of Detection Of Salmonella
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1.58; Pred. No. 0.53;
e 0; Mismatches 36; Indels 0; Gaps
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ucleotides 15735 through 24701 of SEQ ID NO:2
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Salmonella Sequence, Methods Of Detection
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241 GNAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGTGCT 300
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                                                               62 GTTTTTCCTAIGGAAGCATGTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAA 121
                                                                                                                                                   181 ACTGATGCATTATGCTGGATACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTA 240
                                                                                                                                                                                                                                       182 ACTOANGONTANGCTGGATACCCATTTTTGTACTGAATTTCTTTCACTGCTTCAGGTA 241
                                                                                                                                                                                                                                                                                                                           242 GAAATACCAGGTACCAGTAACCTCTTGGGTAGTGATTTTATTGTGCCCCATTAACAGTGCT 301
                                                                                                                                                                                                                                                                                                                                                                                      301 TTGBACCCAATTCTCTATACTCTGAGCAGAGCATTTAAAGAAATGATTCATCGGTTT 360
                                                                                                                                                                                                                                                                                                                                                                                                               361 TGCCATAACTACAGAAAAAAAATCTATGGACAGCAAAGGTATCAGAAAACATATGCTC 420
2 GCCCAGATITATICAGIGGCAATITITCTIGGTATTAATTIGGCCGCATTIATCAICAIA 61
                                                                                                                              21 STACGGAATCAAGTTAAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTT
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IIILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUERRY APPLICATION NUMBER: US/09/989,442
CUERRY FILLING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/179,065
PRIOR FILING DATE: 2000-01-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR PETATOR NOW NEWS. 60,740,628
PRIOR PLILIED DATE: 2000-12-40,86
PRIOR PLILIED DATE: 2000-12-44,86
PRIOR PLILIED DATE: 2000-16-28
PRIOR PLILIED DATE: 2000-16-38
PRIOR PLILIED DATE: 2000-17-11
PRIOR PLILIED DATE: 2000-17-11
PRIOR PLILIED DATE: 2000-17-11
PRIOR PLILIED DATE: 2000-18-14
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PRIOR FILING BATE: 2000-07-26
PRIOR PRICATION NUMBER: 60/217,496
PRIOR FYLING DATE: 2000-07-11
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PRIOR APPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: 60/225,447
PRIOR FILING DATE: 2000-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/218, 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/225,757
PRIOR FILING DATE: 2000-08-14
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PRIOR FILING DATE: 2000-08-22
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PRIOR FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-08-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 33, Application US/09989442
Publication No. US20030013649A1
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US-09-989-442-33
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                                                                                                                                                                                                                                           Length 530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 4031
                         CURRENT FILING DAFE: 2001-01-17
PPIOR application data removed - consult PALK or file wrapper NUMBER OF SED ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPRENCE: PCHOS
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llarity 96.6%; Pred. No. 6.9e-111;
Conservative 1; Mismatches 13;
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ilarity 96.6%; Pred. No. 6.9e-111;
Conservative 1; Mismatches 13;
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    CURRENT APPLICATION NUMBER: US/09/764,853
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Patent No. US20020147140A1
GENERAL INFORMATION:
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US-09-764-853-137
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Matches 458; Conserv
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LENGTH: 530
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                                                                                                                 SEQ ID NO 137
LENGTH: 530
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60/235, 834 60/234, 274 60/234, 274 60/234, 274 60/224, 232 60/224, 519 60/224, 519 60/241, 809 60/241, 809 60/24	(1) (2) (2) (3) (4) (4) (4) (4) (4) (4) (4) (4) (4) (4
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PRING PRING NUMBER: 60244, 532

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240 AGNAATACCAGGIACCAFAACCTCTIGGGTAGTGATTGGTTATTCTGCCATTAACAGTGC 299
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APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TITLE OF INVENTION: CONFOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: FREMEMBER AND DIAGNOSIS OF BREAKY CANCER
TITLE OF INVENTION: PREMEMBER AND DIAGNOSIS OF BREAKY CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37.8; DB 3; Length 1265;
Pred. No. 0.47;
0; Mismatches 87; Indels 0;
                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Potter, Jane E. R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/991,789A
FILING DATE: 11-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-08-991-789A-169
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INPORMATION FOR 800 1D NO: 168: SOURCE CHARACTERISTICS.
LENGTH: 1265 Dade pairs
TYPE INCLECT CACL CACL
STRANDENGES: SINGLE
STRANDENGES: SINGLE
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 6344550
                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: <URKDOWN>
ATTORNEY/AGENT INFORMATION:
                                COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TIPE: Floppy disk
                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
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Il Similarity 50.8%;
90; Conservative (
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CLASSIFICATION:
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      STATE: Washington
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APPLICATION NUMBER: US,
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CORRESPONDENCE ADDRESS:
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NEDIUM TYPE: Floppy of
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Best Local Similarity
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US-09-062-451-169/c
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PERLOLIN: News, TK.1, Saffer, J.D.

FILE OF INVENTION: A Salaronalia Sequence, Mechada Of Detection

TILLO OF INVENTION: Of A

TILLO OF INVENTION: Salaronalia Sequence, And Methada Of Detection Of Salaronalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
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Best Local Similarity 38.5%; Pred, No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35; Indels
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                                      22798 AAGAGITITITATGARAITITITACTCITATACTAT 22763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 AACGITITITICITIAIAGIALITACIGAIGCATTAI 193
158 AACGITTITICITIAIAGIAITTACIGAIGCAITAI 193
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STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word Processor (WordPerfect 5.1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WORSEN WE SOUCHWARD V. V. ADDRESS: ADDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/853,659A
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                                                                                                                                                                                                                                       Sequence 61, Application US/08853659A
Patent No. 5925522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single stranded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, John M.
Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEC ID NO: 61:
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CORRESPONDENCE ADDRESS:
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LENGTH: 24701 bases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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STATE: Washington
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE:
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                                                                                                                                                                       RESULT 10
US-08-853-659A-61
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                                                                                                                                                                                                                                                                                                                    300 TITGAAGCCAATTCTCTATACTCTGACACAAAAGACCATTTTAAAGAATGATCATCGGTT 359
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                                 Score 37.8; DB 4; Length 1265;
Pred. No. 0.47;
0; Mismatches 87; Indels 0;
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Pred. No. 0.47;
0; Mismatches 87; Indels 0.
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Title OF INVENTION: COMPOSITIONS AND MICHODS FOR THE
TITLE OF INVENTION: TREATHENT AND DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.41905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1997-04-09
EARLIER APPLICATION NUMBER: PCT/US97/00485
EARLIER FILING DATE: 1997-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: US 99/062/451
EARLIER PETING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILTING DATE: 1997-12-11
EARLIER APPLICATION NUMBER: US 08/489,762
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BARGIRE FILING DATE: 1996-01-01
NUMBER OF SEQ. ID NOS: 312
SOFTWARE: PatrEEQ for Windows Version 3.0
SEQ. ID NO. 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/289,198
CURRENT FILING DATE: 1999-04-09
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EARLIER FILING DATE: 1996-08-20
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; Sequence 1232, Application US/09134001C
; Patent No. 6380370
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Patent No. 6586570
GENERAL INFORMATION:
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                                        Duery Match 8.0%;
Best Local Similarity 50.8%;
Matches 90; Conservative C
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US-09-289-198-169
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Sest Local 8
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SMALL, JOAD M.
ROMG, STATU, JOAD M.
TITLE OF INVERTION: COMPOSITIONS AND WENDODS FOR FREE
FREENWERT ON: COMPOSITIONS AND DISAGNOSIS OF SERAST CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.0%, Score 37.8; DB 4; Length 1265; BB est Local Similarity 50.8%, Pred. No. 0.47; Matches 90; Conservative 0; Mismatches 87; Indels 0; Matches 90; Conservative 0; Mismatches 87; Indels 0;
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STREET: 701 Fifth Avenue, Suite 6300
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FILING DATE: 20-Jun-2000
CLASSIFICATION: <URNOWN>
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SEQUENCE DESCRIPTION: SEQ ID NO: 169:
US-09-598-326-169
NAME: Maki, David J. 1392
REFERENCE/DOCKET NUMBER: 210121.41902
TELECOMENTICATION INFORMATION:
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REGISTRATION NUMBER: 33,332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELENX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 169, Application US/09598326
Patent No. 6423496
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INPORMATION:
                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INPORMATION FOR SEQ ID NO: 169:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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STATE: Washington
                                                                                                                                                                                                                                                                                   LENGTH: 1265 base pairs
                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
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Fri Sep 26 08:42:39 2003

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APPLICANT: IDNO, HENGY T.
TITLE OF INDUSTRICAN EN-USED SOURCE CONSTITUTIVELY ACTIVATED HIMM
TITLE OF INVESTION: No. 1950013165148A1-Endogenous, Constitutively Activated Himm
TITLE OF WINDRICOR: Receptors
                                                                                                                                                                                    CCCAGATTAFTCAGTGGCAATTTTCTTGGTATTAATTTGGCCGCATTATCATCAGCGG 438
                                                                                                                                                                                                                                                                                       62 ITTTICCIAIGGAAGCAIGITTIAIAGICIICAICAAAGIGCCAIAACAGCAACIGAAA 121
                                                                                                                                                                                                                                                                                                                                                         122 TACGGAATCAAGTTAAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTA 181
                                                                                                                                                                                                                                                                                                                                                                                      182 CTGATGCATTATGCTGGATACCCATTTTGTAGCGAAACCTCTTTCACTGCTTCAGGTAG 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 AANTACCAGGIACCAIAACCICTIGGGIAGIGAIIGGIIAAIICIGCCATIAACAGIGCIT 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 AAATACCAGGTACCATAACCICITGGGTAGTGATTITTATICIGCCCATTAACAGTGCTT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 TGAACCCAATTCTCTATACTCTGACCACAAGACCATTAAAGAAATGATTCATGGGTTTT 361
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                                                                                                                                                            2 CCCAGATITATICAGIGGCAATITITICITGGTATTAATITIGGCGCATITATCATCATAG
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                                                                                                            2; Gaps
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                                                        DB 10; Length 612;
                                                                                                            14; Indels
                                                        92.1%; Score 436.6; DB 3
96.6%; Pred. No. 3e-110;
14ve 0; Mismatches 14
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THIS REPRESENT. ASSORDS.

CHORARY APPLICATION DAYS. 2002-21-46

BRICHARD APPLICATION PROSES. 1957-11-46

BRICHARD APPLICATION PROSES. 1957-11-40

BRICHARD APPLICATION PROSES. 1959-11-17-46

BRICHARD APPLICATION PROSES. 1959-11-17-46

BRICHARD APPLICATION PROSES. 1959-11-17-46

BRICHARD APPLICATION PROSES. 1959-11-16

BRICHARD APPLICATION PROSES. 1957-16

BRICHARD APPLICATION PROSES. 1957-16

BRICHARD APPLICATION PROSES. 1957-1951

BRICHARD APPLICATION PROSES. 1957-1951

BRICHARD APPLICATION PROSES. 1957-1951

BRICHARD APPLICATION PROSES. 1959-12-13

BRICHARD APPLICATION PROSES. 1959-13-13

BRICHARD APPLICATION PROSES. 1959-13-13
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PRIOR FILING BAPE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/181,749
PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/10321807
Publication No. US20030166148A1
GENERAL INFORMATION:
                                                                                                        Matches 457; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Chen, Rupong
                                                                                     Sest Local Similarity
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              13-09-895-686-37
                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.3%; Score 437.6; DB 14; Length 1126; BB set Local Similarity 96.6%; Pred. No. 2.2e-110; Matches 458; Conservative 0; Mismatches 14; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20020106655A1 2488822X308B1
                                                                                                                                                                                                  OTHER INFORMATION: Incyte ID No. US2003012005781 3556218CT
                                                                                                                                                                                                                                                                                                                             0; Mismatches
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APLICONN: Tong, Y. Ton
APLICONN: Days, Y. Ton
APLICONN: Days, D. Ton
CHERK PRESENCE: PC-0444 CLF PC-12108
FILE METABLES: PC-0444 CLF PC-12108
CHERK PARTACATION NURBER: 190/9/95,666
CHERK PARTACATION NURBER: 190/9/95,666
SHERKE FILING AND: 2001-06-28
SHERKE ELING AND: 2001-06-28
SHERKE FILE PC-9240
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Patent No. US20020106655A1
NUMBER OF SEQ ID NOS: 305
SOFTWARE: PERL Program
SEQ ID NO 255
LENGTH: 1126
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                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
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                                                                                                                           ORGANISM: Homo sapiens
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LOCATION: 561
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                                                                                                   TYPE: DNA
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1729 ATCTGCTGGATTCCTGTATTTGTAATTAAAATCCTTTCCCTCTTCCGGGTGGAAATACCA 1788
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                                                          70 IATGGAAGCATGTTTATAGTGTTCAICAAAGTGCATAACAGCAACTGAAATACGGAAT 129
                                                                                                                                                                                                                                 130 CANGTTANAAAAGAGATGATCCTTGCCAAACGTTTTTTCTTTATAGTATTACTGATGCA 189
                                                                                                                                                                                                                                                                                                                                                                                                         190 TIAIGCTGGAFACCCATTTTTGTAGCGAAACCTCTTTCACTGCTGGTAGAAATACCA 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 INTGGARGCATGTTTTATAGTGTTCATCAAAGTGCCATAACAGCAACTGAAATACGGAAI 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               310 ATTOTOTATACTOTGACCACAAGACCATTTAAAGAAATGATTCATCGGTTTTTGGCATAA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT FERRY, J. N.
APPLICANT, RERRY, J. N.
APPLICANT, RAMANTER, C. S.
APPLICANT, RAMANTER, C. S.
APPLICANT, RAMANTER, C. S.
TITLE OF INPRITUEN, RAVOREL DAMA C-PROTEIN COUPLED RECEPYOR, REPRESENT, C. TITLE RESERVED, C. OLLINGTON, RECEPYOR, RECHEL TH. SPAIN AND OTHALIA TISSUES
CORRENT PRILIARO DARRES, 1001-109-58, 255A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O; Gaps
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Pred. No. 5.9e-37;
0; Mismatches 117; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHREME TILLED DATE: 2001-09-25 PRIOR APELICATION NUMBER: 60/215,713 PRIOR PETIND DATE: 2001-09-27 PRIOR APELICATION NUMBER: 60/215,713 PRIOR APELICATION NUMBER: 60/215,713 PRIOR APELICATION NUMBER: 60/210,713/06-60 PRIOR PETING DATE: 2001-09-20 PRIOR PETING DATE: 2001-09-20 PRIOR PETING DATE: 2001-09-30 P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09965536A
Publication No. US20030027323A1
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al Similarity 67.4%;
242; Conservative (
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US-09-965-536A-5
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LENGTH: 2142
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PRIOR FILING DAMPS: 2000-08-10
NUMBER OF SEQ ID NOS: 42
SOFFWARE: Patentin Ver: 2.0
SSSD ID NO II.
                                         SOFTWARE: Patentin version 3.0
SEQ ID NO 17
LENGTH: 1068
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NUMBER OF SEC ID NOS: 133
                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-09-928-175-11
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Search completed: September 25, 2003, 15:11:48 Job time : 191 secs

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AAU38931
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N-PSDB; AAF28059.
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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AAY42171
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                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score: 826
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07-JUL-2000;
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     The present invention provide the protein and coding sequences for a nowel, hear of protein compile tempetor, destinant SELLIGIT. The sequence are useful, in the disposite prevention and fractions of diseases are useful. In the disposite percention and fractions of diseases are part and a sequence search on the sequence search of the seases, even bett failure, proteins, supplies a partitions of states, even bett failure, proteins, supplies and the sequence search of the sequence search of the sequence of 
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Novel G-coupled protein receptor, HGRL101 useful for treating diseases such as microbial infections, cancers obesity, asthma, disbetes, howotension, strong as second size movemental infarction, strong, ulcar.
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antiparasitic; acatlant; immune discoter; acatlovascular discoter;
neurological disease; infection; nephrotropic; que therapy; vaccine
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100.0%; Pred. No. 1.3e-88;
tive 0; Mismatches 0;
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                                                                                                                                                Claim 1; Page 36; 36pp; English.
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2000US-0190076,
2000US-0198123,
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04-FBB-2000;
24-FBB-2000;
02-MAR-2000;
16-MAR-2000;
18-APR-2000;
18-APR-2000;
19-MAY-2000;
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isolated from a range of human tissues disclosed in the specification
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Satches 127; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 638; DB 21; Length 396;
Pred. No. 4.7e-66;
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                                         Claim 1; Page 62-63; 71pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 WHNYRORKSMDSKG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 WYNYRORKSMDSKG 348
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cardiovascular disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human G protein coupled protein receptor peptides useful for the prevention, diagnosis and treatment of cell proliferative, neurological and immune disorders -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guegler KJ,
disorders e.g. neoplasms of the breast or liver,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 638; DB 22
Pred. No. 2e-66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baughn MR;
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neurological disorder, immune disorder; cytostatic; pancreatic cancer; follicular carcinoma of the thyrold; leiomyoma of the uterus; epilepsy; interstital nephritis; cancer.
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fagnosis, prognosis, treatment and evaluation of therapies for
nechyatic, neurological and immune disorders
                                                                                                                                                                                                                                                                                                                                                     Human; G-protein coupled receptor; GPCR; necplastic disorder;
                                                                                                                                                                                                                                                                                                            Juman G-protein coupled receptor #4, Incyte clone 2488822CD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seoplastic, neurological and immune disorders
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                                                                                                                                                                                           ABU54868 standard; Protein; 396 AA.
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335 WYNYRORKSMDSKG 348
                                                            121 WHNTRORKSMDSKG 134
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(LALP/) LAL P G.
(TANG/) TANG Y T.
(BAUG/) BAUGHN M R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bandman O, Lal PG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI: 2002-697866/75.
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                                                                                                                                                                                                                                    MAKENEK M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to business greater, coups at second categoric (acts) and their accessoration for maintenance of course and course or the course of course or the course or 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dementia. The invention also provides geneite careaning procedures that catcaining a person's genome with respect to GFGs. The vectors are useful for the secondinant production of the GFGS, a present sequence is man coAR22 & protein-compled receptor (GFGS) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seven transmembrane receptor polypeptides and polynucleotides, useful 
for treating menotodida, no psychiatric disorders, e.g. solizophremia, 
as well as for identifying compounds useful for treating schizophremia
                                                                           /label= Transmembrane_domain_(5TM)
                                                                                                                                                                        /label= Transmembrane_domain (6TM)
                                                                                                                                                                                                                                                                  /label= Transmembrane_domain_(7TM)
                                                                                          242..267
/label= Intracellular_domain
/note= "Third IC loop"
                                                                                                                                                                                                          /label- Extracellular_domain
/note= "Third EC loop"
                  'label= Extracellular_domain
                                     /note= "Second EC loop"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 15-16; 215pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PHAM ) PHARMACIA & UPJOHN CO.
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99US-0429555.
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99US-0429695.
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28-0CT-1999;
28-0CT-1999;
28-0CT-1999;
03-DEC-1999;
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27-0CT-1999;
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The invention originates to maintain down concile operation on the invention original conciles for the complex of the complex operations and the complex of the complex operations are inventionally of the complex operation of the complex operations of the complex operation of the complex of the complex operation of the complex of the c of the uterus, panoreatic cancer, epilepsy, interstitial nephritis and immune response as a complication of cancer. The present sequence is a human effect to the invention. 396 AA; Seguence

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77.2%; Score 638; DB 23; Length 396; 94.8%; Pred. No. 4.7e-66;

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Score 638; DB 22; Length 396; Pred. No. 4.7e-66; 1; Mismatches 6; Indels (

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the present sequence represents the human of procusts monopolar exemptor the market and 
                        576 AOIYSVAIFLGINLAAFIIIVFSYGSMFYSVHOSAITATBIRNQVKKEMILAKRFFFIVF 635
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94.8%; Pred. No. 1.1e-65;
tive 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Der Spek PJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 3; 54pp; English
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                                                                                                      L21 WHNYRORKSMDSKG 134
                                                                                                                              20-DEC-1999 (first entry)
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                                                                                                      TOALCWIPIPVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPPKEMIHRF 120
                                                                                                                              275 TDALCHIEFTVKFLSLEGVEIRGITSSWYTEILPINSALNPILYTYTYREBKIHRE 334
                             AQIYSVAIFIGINLAAFIIJVESYGSMEYSYBOSAI%AFERNOVKKEMILAKREFETVE 274
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1 ACIYSVAIFLGINLAAFILIVFSYGSMFYSVHOSALTATEIRNQVKKEMILAKRPFFIVF 60
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Pred. No. le-65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human LGR7 short form protein sequence.
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N-PSDB; AAZ25346.
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Best Local Similarity
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Score 638; DB 24; Length 757; Pred. No. 1.1e-65; 6; Indels

1; Mismatches

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576 AQIXSVAIPLGINIARFILIVESYGSMFYSVRQSAITAFEIRMQVKKEMILAKRFFFTVF 635
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 TDALCWIPIFVAKPLSILQVBIPGFITSWVJGYSAINSALNPILYTLTRPFKEMIHRF 120
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any other disorder in which Greek are involved, the entitlodies may be used in immunoassays and immunodiagnossis. ARA4252 to ARA42866 encode Special offers in ARB843866 encode szept) that ARB843868 encode szept) that ARB843868 encode szept) that the tressent invention of the present invention.
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respiratory disorder; renal disorder Kidney failure; blood disorder;
myoenclafi infarction; wound dealing; cell proliferation; skin agine;
food additive; food preservative; gene therapy.
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16-MAR-2000, 20000S-018974
17-MAR-2000, 20000S-0190076
18-MS-2000, 20000S-019012
19-MY-2000, 20000S-020515
07-TRI-2000, 20000S-0209467
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                                                                                                                                                                                                                                                                                              Local Similarity
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30-JUN-2000;
07-JUL-2000;
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                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wew isolated antigenic peptides e.g., for G protein-coupled receptors (GPCR), useful for disproating and designing dusys for threating conditions in which GPCEs are involved, e.g., AIDS, Alzhaimer's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein-coupled receptor LGR7 protein SEO ID NO:623
                                                                                                                                                                                                                                                                                ABP81724 standard; Protein; 757 Ab.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LIPE-) LIPESPAN BIOSCIBNOBS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burmer GC, Roush CL, Brown JP;
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                           121 WHNYRORKSMDSKG 134
                                                                                                        696 WYNYRORKSMDSKG 709
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N-PSDB; AB242570.
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acute kidhey fallure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to present skin ading due to sunburn, to maintain organs before transplantation, for supporting cell culture of
                                                                                                                                                                                                      primary tissues, to regenerate tissues and in Chemicaris. The properties of the state of the sta
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 75.34; Score 532; DB 22; Length 176; Dest Local Similarity 94.04; Pred. No. 8.3ee 6; Matches 125; Conservative 1, Mismatches 7; Indels 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human musculoskeletal system related polypeptide SEQ ID NO 2009.
                                                                                                                    Length 176;
                                                                                                                                                                       7: Indels
               from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                    Score 632; DB 22;
Pred. No. 8.3e-66;
                                                                                                                                                                       1: Mismatches
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including digestive system cancers and also for testing and detection
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epilopsy; and (f) infectious diseases e.g. oestebral anoxia and
and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated digestive system associated polypeptide for treating,
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08-8WY-2000; 200089-028-55.

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The infections contain the patent did not form part of the printed specification, but was obtained a lactronic formst directly printed specification, but was obtained in a lactronic formst directly printed specification. Isolated polypeptide for treating, preventing and/ or prognosting disorders related to the misouloskeletal system including musouloskeletal cancers and also for testing and detection e.g., diagnosis. Claim 11; SEQ ID NO 2009; 781pp + Sequence Listing; English. :HS 08 - 8 - 700 - 500 Rosen Ch. Barash SC. Ruben (HUMA-) HUMAN GENOME SCI INC WPI; 2001-451937/48. N-PSDB; AAL35644.

176 AA:

Sequence

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20000S-228924P.
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   Score 632; DB 22; Length 176;
Pred. No. 8.3e-66;
                                       Indels
                                   1; Mismatches
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2000US-225447P.
2000US-225757P.
Query Match 76.5%;
Best Local Similarity 94.0%;
Matches 126; Conservative 3
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Ruman; uterine motility-association disorder; uterus; pregnancy;
                                                                                  Novel human uterine motility-association polypeptide #15.
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2000US-0232400
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                                           21-NOV-2001 (first entry)
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                                                                                                                                                                                                    Homo sabiens.
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AAU18108;
61 TDALCWIPIFVARPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFREMIHRF 120
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             (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; SBQ ID No 84; 524pp; English.
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08-DEC-2000; 2000US-0251866.
08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251999.
11-DEC-2000; 2000US-0251990.
05-DRI-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC
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                                                                                                         Rosen Ca, Barash SC, Ruben SM;
                                   (HUMA-) HUMAN GENOME SCI INC.
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N-PSDB; AAS29573.
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Query Match (5.5%) SCORe 532; DB 22; Length 1/5; Best Local Similarity 94.0%; Pred. No. 8.3e-66;	Indels	1 AQIYSVAIFLGINLAAFILIVFSYGSKFISVHQSAITATBIRNQVKKEMILAKRFFEIVF 60	1 AQIYSVALFLGINLAAFILIVPSYGSMFYSVHQSALTATEIRNQVKXEMILAKRFFFLVF 60	61 TDALCWIPIEVAKPLSLLQVEIPGTITSWVIGYSAINSALWEILYTHTRERHIRF 120	61 TEALCMIPIEVVKFLSLLQVEIPGTITSWVIFILPINSALMPILYTLTRPFKEMIRFF 120
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Copyright (c) 1999 - 2003 Compugen Ltd.  OR nucleic - nucleic search, using av model Run on: september 25, 2004, 13:06:05; search time 1645 seconds Titles: US-10-049-568-1 f00.05; search time 1645 seconds Titles: US-10-049-568-1 f00.05; search time 1645 seconds Total number of Nice satisfying chosen parameters: 45562784 Minimum Do seq length: 0 capert 1.0 Searched: 12761329 seqs, 12151238056 residues Wilnium Do seq length: 0 capert 1.0 Maximum Do seq length: 0 capert 1.0 Maximum Do seq length: 0 capert 0 capert 1.0 Maximum Do september 1.00000000 Post-processing Maximum Match 100 Post-processing Maximum M	Database : NSS:	17. State Section 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	Pred. No. is the number of results predicted by chance to have a card is deliced by analysis of the rotal core edstmint build printed, and a general busing the core of the rotal core edstmint.  Superior of the core of the rotal core edstmint of the core of t

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603866563FI CSECCHN54 Gallus gallus CDNA clone ChEST886m16 5', mRNA
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                                                                                                                                                                         /mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                 /ordanism-"Gallus gallus"
        Simon. Hubbard@umist.ac.uk
                                                                                                                                                                                                                                                                                                                                           /sex="Female"
/tissue_type="cerebrum"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                   /clone="ChEST489a19"
                                Location/Qualifiers
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Fong, M.T., Tickle, C., Eroem, N. R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken chNks
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Bost Local Samilarity 95.43; Pred. No. 7.9e-52.

Matches 330; Conservative 0; Missarchies 16; Indels 0;
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Proc. Nell. Aced. Sci. U. S. 8.9 (19), 12257-12252 (2002).
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66.3%; Pred. No. 2e-09;
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5841 S. Maryland Ave., WC2115, Chicago, IL 60637, USA
7841: 773-702-6788
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Best Local 5
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                                                                                                                                                                                                  /Cissue_type="tterus"
//der_stage="honarial day 14"
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//der_organ: uterus, CDM qenerated by PF-TCR from total
//MSNe Artacked from poctsine meanatal uterine tissue."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            178 TTRACTGNTGCATTATGCTGGNTACCCATTTTTGTAGCGAAACCTCTTTCACTGCTTCAG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       238 GTAGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGTTATTCTGCCATTAACAGT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      298 GCTTTGANCCCAATTCTCTATACTCTGACCACAAGACCATTAAAGAAATGATTCATCGG 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.2 GCCTTGAACCCAATCCTCTACACTCTCAACCACTTTTTCAAGGACACATGAACAG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 TICICIGAGACACCAGATACCCGTAFTGTCATTANAATTCTCTCCCCTTTCCGG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Būkaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 197)
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h Mg1-throughbut GEG1 procedure for converting large number of
8AGB tag sequences into 3, ESTs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tissue_type="bone marrow" /cell_type="cbl5+ myeloid progenitor cells" /cell_type="cbl5+ myeloid progenitor cells cDNA /clone_lib="human cbl5+ myeloid progenitor cells cDNA
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5841 S. Maryland Ave., MC2115, Chicago, IL 60637, USA
Tel: 773-702-6788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19.0%; Score 90; DB 14; Length 198;
Lilarity 66.5%; Pred. No. 5.8e-10;
Conservative 0; Mismatches 65; Indels
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/mol_type="mRRA"
'organism" Sus scrofe"
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/db xref-"taxon:9823"
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                                                                                                                                                           /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 TITIGGCAIRACIA 371
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Best Local Similarity
Matches 129; Conserve
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Single pass sequencing. Bases called and trimmed with phred vol96094. Westor identified by cross_match with the "missore 20 and "minatch 12 options." FOR FRIENCE TO FER FRIENCE TO FORMARIO CONTRIBUTION.
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158 bp marks linear EST 08-JAN-2003
1587 1678 Sus scrofs meomatal sterns FF-PCR Sus scrofs cDWA clone
CASS/Similar to Porcine LGR8 (1851) feeeppor), mWN sequence.
CAST/681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      160 CGITTITITCTTATAGTATTTACTGATGCATTATGCTGGATACCCATTTTTTTAGCGAAA 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              220 CCTCTTTCACTGCTTCAGGTAGAAATACCAGGTACCATAACCTCTTGGGTAGTGATTGGT 279
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//Barrentana..
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1 (bases 1 to 199)
Bartol,F.F., Wiley,A.A., Bathgate,R.A.D. and Bagnell,C.A.
INSI3 receptor (LRN) expression by mematal porcine uterine
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Sequence of CDNA (198 pp) generated by RT-FCR from total RNA
extracted from pocine neonstal uterine tissues obtained on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.8%; score 98.4; DB 9; Length 235;
66.5%; Pred. No. 7.5e-12;
1ye 0; Mismatches 71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               340 AAAGAAATGATTCATCGGTTTTGGCATAACTA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 AAGGACACGTTGAACAGCTGCTGCACAACCA 216
Small: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
                                                                                                                                                                                    BACKWARD: GITITOCCAGTCACGACG
Plate: 34 row: F column: 22
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                        /mol_type""mRNA"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .235
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Sus scrofa
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                                                                        Sukaryota, Metazoa, Chordata, Cranlata; Vertebrata; Buteleostomi;
Mamanla; Butheria; Cetarthodactyla; Suina; Suidae; Sus.
I (pases 1 to 235)
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USDA, ANS, US West Animal Research Center
PO Box 166, Clay Center, RE 68933-0166, USA
TPM: 402 752 4366
Fbx: 402 763 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 130; DB 9;
Pred. No. 5.6e-19;
'organism="Silurana tropicalis"
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Matches 230; Conservative
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Page 9

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## GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 25, 2003, 14:59:01 on:

1; Search time 19 Seconds (without alignments) 794.657 Million cell updates/sec

1 AQIYSVAIFIGINLAAFIII.........HMLHHSSGGKCGHCRRCHLS 157 Title: US-10-049-568-2 Perfect score: 826 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283308 segs, 96168682 residues

Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

plr2:** PIR 76:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

follitropin recept 3 protein-coupled follitropin recept lutropin-chorlogon follitropin recept Collicle Stimulati follitropin recept luteinizing hormon utropin-choriogon thyroid stimulatin thyroid stimulatin follitropin recept lutropin-choriogen probable G protein adenosine receptor hyroid stimulatin follitropin recept follitropin recept hyrotropin recept hyrotropin recept thyrotropin recept A2-adenosine recep alpha-1-adrenergic alpha-1B adrenergi adenosine receptor protein-coupled protein-coupled Lutropin receptor Description A40077 540241 JC1493 JC2033 JN0898 A41344 A41344 I45896 A42395 JC7389 JC7361 A35956 148933 840491 368678 JC5643 830341 Query Match Length DB Score 207.5 143.5 143.5 141.5 130.5 139.5 136.5 134 . Ю Result

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Indels 33: DB 2: Length 1115; 25.1%; Score 207.5; DB 2 33.1%; Pred. No. 6.9e-13; ive 25; Mismatches 45; Best Local Similarity 33.18 Query Match

Gaps

61 TDALCMIPIEVARPLSLLOVEIPGTITSWVVIGYSAINSALNPILYILITREP----- 113 38 YSVGVFILLNILSFVLIASSYLMMF-SVAKKTRSAVRTARSKN----DNAMARRWILLVM 992 4 YSVAIFLGINLAAFIIIVFSYGSMFYSV---HQSAITATEIRNQVKKEMILAKRFFFIVF 60 용 ö ö

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A:Note: the authors translated the codon AGT for residue 488 as Arg
C:Punction:
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33.3%; Pred. No. 2.1e-06;
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1 Similarity 27.2%; Pred. No. 1.4e-06;
44; Conservative 32; Mismatches 59.
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A. Residues: 1-695 <KHA
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TITLS OF INVENTION: POLYBEPTIDES OF G-COUPLED PROTEIN
TITLS OF INVENTION: RECEPORS, AND COMPOSITIONS AND METHODS THEREDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
16.5%, Score 136; DB 1; Length 370;
Gest Local Similarity 28.5%, Pred. No. 8.1e-07;
Matches 39; Conservative 24; Mismetches 50; Indels ;
Matches 39; Conservative 24; Mismetches 50;
COMPUTER: IBM PC compatible
OPENATING SYSTEM: DC-105/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION 19A7A:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDING TETE: FLORE OF CHARACTERS. IMP PC CORPARIS. CORPERATION SYSTEM: PC-TOS/MS-DOS SOFTWARES: PW-CHARACTER SALEMSE PT.10, Version #1.35 CHRENAT APPLICATION MAYA. PREP. 197939/08528 TILING DAYE: 09-589-1993
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STREET: 419 Seventh Street, N.W., Suite 300
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FILIND DATE: 110-828-1992
ATTORNEN' AGENT INFORMATION:
NAME: PROMADOMEN, AGENT ON THE SERVICE OF THE SERVI
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FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                             APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
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Sequence 18, Application PC/TUS9308528
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 370 amino acids
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 SQUYILSILIRATHCGLNUVAFVVICACYIRIYFAVQNPELFAP-----NKDTKIAKKM 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 FFIVFIDALCWIPIFVAKPESILOVB-----IPGFITSWVJGYSAINSALNFILTT, 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109 TTRPEKE-----SMDSKGIRK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AQIYSVAIFL----GINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRF 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Owery Match 16.6%; Score 137.5; DB 3; Length 795;
Back Local Similarity 21.9%; Pred. No. 1.4e-06;
Matches 43; Conservative 38; Mismatches 64; Indels 51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Murphy, Randell B.
APPLICANT: SCHEREF, David I.
APPLICANT: SCHEREFILES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPPORS, AND COMPOSITIONS AND METHODS THEREOF
                                                                                                                                                                                                                                                                                                                                 COMPUTE: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: BROWDY AND NEIWARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
CONYREY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 91913/1107/US/ST
                                                                ADDRESSE: CUSHAN DARBY & CUSHMAN STREET: 1615 I STREET, N.W. CITY: WASHINGTON, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/07/741,453A
FILING DATE: 19911015
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Patent No. 5508384
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TELEPRONE: (202) 861-9004
TELEX: 6714627 CUSR
TELEX: 6714627 CUSR
TEMPORATION FOR SEQ ID NO: 55:
SEQUENCE CHRANCTRRISTICS:
LENGTH: 755 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              773 -- LSTVRATHOGHCQQ 786
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NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 1677
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MEDIUM TYPE: Floppy disk
NUMBER OF SECUENCES: 62
                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
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US-07-741-453A-55
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Disk
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                                                                                                                                                                                         COUNTRY: U.S.A.
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TRLECOMMUNICATION INFORMATION-

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528 SOVYISTIT-LANDAPPOVICACYTRIVENCOMPRITAD----NKDTKIAKKMAILIF 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             581 TDFTCKAPISFPISAAFKVPLITVTNSKILLVLFTPVNSCANPFLYAIFTKAFORDFL. 640
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                                                                                                                                                   12;
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            Ouery Match 16.2%; Score 134; DB 3; Length 700; Beet Local Similarity 27.3%; Pred. No. 2.9e-06. Metches 34; Conservative 31; Mismatches 48; Indels Metches 34; Conservative 31; Mismatches 48; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
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APPLICATION DATA:
PLING DATE: 10-8ep-1991
CLASSIFICATION: (Thrown)
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### MOLECULE TIME: PROTEIN |
### SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-07-57-3420-8
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TELEPRONE; (617)523-3400
TELEPRONE; (617)523-6440
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TELEPRONE; (617)523-6440
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TELEPRONE; (617)523-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8, Application US/07757342D
Patent No. 6218509
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: IGARASHI, Masac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Massachusetts
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 MIHRF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                237 LEKESBEKKAAKILGIVOGHILGHIPPETALPIGSILESTIKEPDAVEKBEHGY--FUSC 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 16.5%; Score 136; DB 5; Length 370; Best Local Similarity 28.5%; Pred. No. 8.1a-07; Independent 39; Conserveive 24; Mismatches 50; Indels
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APPLICANT: IGARGEI, Masao
MAKAMUTA, RAZUTO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 41226
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REGISTRATION NUMBER: 31003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 130 Water Street
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TELEFAX: (617)523-6440
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TELEFAX: 126657, -
INTORMATION POR SDD ID NO: 18:
SEGURAR CHARACTESTICS:
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SEQUENCE CHARACTERISTICS
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CORRESPONDENCE ADDRESS:
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MOLECULE TYPE: protein
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TOPOLOGY: linear
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Richa, T.; Hirai, T.; Yoshiura, Y.; Kobayashi, T.; Wagahama, Y.
Biocham, Brodyrs, Res. Comm. 276, 258-258; Johnson, P. Stariession of thyrotropin recepto
Ajritie: Cloning, Res. Commandation, and expression of thyrotropin recepto
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C. Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane protein
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Keywords: glycoprotein; hormone receptor; thyroid gland; transmembrane protein
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NAlternate anassi thyrotropin receptor a
Species Oncohynchus Sp. (Salmon)
Sp. (Species Oncohynchus Sp. (Salmon)
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1 Similarity 26.8%; Pred. No. 1.5e-05;
44; Conservative 32; Mismatches 60; Indels
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A; Contents: Thyroid
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                                                          116 MIHRF 120
                                                                                                                                                           641 LLSRF 645
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F.661.64/Finding Site: phosphate (Sys) (covalent) #status experiments
F.607/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predirte
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             Bicchem. Biophys. Res. Commun. 172, 1049-1054, 1990
A;Titls: Cloning and Sequencing of human InfroG receptor
A;Reference number: A56243, MUD:91058534, PMID:2244890
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AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATBIRMQVKKEMILAKRFFFIVF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               539 ILSKPGCYEMOAQLYRTETSSTA-----HISHPRNGHC 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            705 R 705
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Best Local Si
Watches 43;
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48; Indels

25; Mismatches

29.68; Conservative

Matches

R;Minegish, T.; Makamura, K.; Takakura, Y.; Miyamoto, K.; Hasegawa, Y.; Ibuki, Y.; Igard

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similarity to other G
protein-coupled receptor transmembrane regions,
hydrophobic, about 20-23 amino acids in length
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COCATON: 45 to 491
INSWITTCHION MERGO: similarity to other G
INSWITTCHION MERGO: protein-complex freeport transmembrane regions,
INSWITTCHION MERGO: Phytopholoc, down 20-23 mains each in leight
INSWITTCHION MERGO: Phytopholoc, down 20-23 mains each in leight
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hydrophobic, about 20-23 amino acids in length
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domains, hydrophilic
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LOCATION: 1 to 349
                                                                                                                                                                                                                                                                                                            COMICTER READABLE PORM:
MUDINA TIPE: 3.5 "disherte, 1.44 MB, high density
COMPUTER: IBM PS/2, model 55 SX
OPREMATIVE SYSTEM: MS-TOW Version 4.0
OFFWARE: WAX/MS MASA1 via Komit to IBW MS-DOS
SOFFWARE: WAX/MS MASA1 via Komit to IBW MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KRY: putative transmembrane region I LOARION 80 to 30 to 30 to 10 INSTRUCTION METHOD: protein complete recept IDENTIFICATION METHOD: protein complete recept IDENTIFICATION METHOD: protein complete about 20.
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LOCATION: 350 to 613
IDENTETCATION METHOD: similarity to other G
IDENTETCATION METHOD: protean-coupled recept
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LOCATION: 382 to 404
IDENTIFICATION METHOD: SIMilarity to other G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity with other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: putative transmembrane region III
LOCATION: 427 to 448
IDENTIFICATION METHOD: similarity to other (
                              ADDRESSER: Stephen P. Williams,
ADDRESSER: Ares Serono, Inc.
STREET: Exchange Place, 37th floor
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hydrophobic
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FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: US/252
TRLECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRICE APPLICATION DATA:
APPLICATION NUMBER: 07/670,085
PILING DATE: 15-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Williams, Stephan P. REGISTRATION NUMBER: 28546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (617) 723-1300
TELEFAX: (617) 723-8923
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: signal sequence
LOCATION: -17 to -1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTIFICATION METHOD:
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LENGTH: 695
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CORRESPONDENCE ADDRESS:
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LOCATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TDALCWIPI-FVAKPLSLLOVEIPGTITSWVJGYSAINSALNPILTTLTTRPFK---- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ADIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
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                                                                                                                                                                                                                                                                                                                                          TITLE OF INVESTION: STRAIGHT OF CLONE DRUGS FOR G PROTEIN
HITHER OF PROFITCH: COUPLED RECEPTORS
HITHER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 LLSKCGCYEMOAQI --- YRTRISSTV ----- HNTHPRNGHC 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 -----EMIHRFWHNYRORKSMDSKGIRKHWLHHSSGGKCGHC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER TREADMINE FORM 418 MENTINE TREE FORM 418 MENTINE TREE FORDY 418 MENTINE TREE COMPUTER. LEE COMPUTER. LEE FORDY FORM 51.00 MENTINE SYSTEM: FORDY 51.00 MENTINE SYSTEM: PRESENTE FORDY 51.00 Wersion #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MIXON, HARGEAUE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICART RAIDON, CHUISTES AND
APPLICART Schedichardt, Rene Unn
APPLICART SCHED, SILIARY VIL Fen
APPLICART NGHORT, NO. 5744456600 PARTICO
TITLE OF INVESTION: Manch POLITICE SIMILATING
TITLE OF INVESTION: Moreon Politice Similating
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIPIONITION: 530
APTONINI/AGENT INFORMATION:
NAME: REMAIN, 5053N J. 3
RESISTRATION NUBBER: 34,103
REPRESSING/CHOT INFORMATION:
TELEPORNINI/CTON INFORMATION:
TELEPORNINI/CTON INFORMATION:
TELEPORNINI/CTON INFORMATION:
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APPLICATION NUMBER: US/08/795,876
                                                                                                                                                                                                                                 APPLICANT: Gershengorn, Marvin C.
APPLICANT: Geras-Raaka, Elizabeth
APPLICANT: Nussenzveig, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/08487886
Patent No. 5744448
                                                                                                         ; Sequence 2, Application US/U8795876
; Patent No. 6403305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         not relevant
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INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                           GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14603
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                                                                           US-08-795-876-2
                                     RESULT 14
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61 TDALCWIPI-PVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFK---- 114
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DONIONIO: 557 to 360
IDSMIRICATION MERIDO: percein-coupled receptor transmembrane regions,
TORNIFICATION MERIDO: percein-coupled receptor transmembrane regions,
TORNIFICATION MERIDO: percein-coupled compose a couple in length
TORNIFICATION MERIDO: perceipendic, about 20-32 maino exists in length
                                                                                                                                                                                                                                                                                                                                                                                                      MANGACE: putative transmembrane region VII
CONTINN'S 25 to 653
INSERTIVATION METHOD: similarity to other G
INSERTIVATION METHOD: sprinciples freedport transmembrane regions,
INSERTIVATION METHOD: hyptopholog, about 20-73 amino exide in length
                                                                  similarity to other G protein-coupled receptor transmembrane regions, hydrophobic, about 20-23 amino acids in length
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15.2%; Score 125.5; D8 1; Length 695;
Seef Local Stallarity 26.1%; Pred. No. 2.ec. 6, 5, 848.8 Matches 43; Conservative 30; Mismatches 59; Indels 33; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 -----EMIHRFWHNYRQRKSMDSKGIRKHMIHHSSGGKCGHC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KET: putative carboxy-terminal intracellular
NAME/KET: domain carboxy-terminal intracellular
NAME/KET: domain carboxy-terminal intracellular
195-08-103-1086-2
NAME/KEY: putative transmembrane region V
LOCATON 512 to 53 to 53
IDENTETATION METHOD: similarity to other
IDENTETATION METHOD: protein-compled rec
IDENTETATION METHOD: hydrophobic, about ,
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Search completed: September 25, 2003, 15:01:14 Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

September 25, 2003, 15:00:41; Search time 64 Seconds (without alignments) 371.175 Million cell updates/sec

1 AQIYSVAIFLGINLAAFIII......HMLHSSGGKCGHCRRCHLS 157 Title: US-10-049-568-2 Perfect Score: 826 Sequence:

Total number of hits satisfying chosen parameters: 556894 segs, 151307093 residues Searched:

Gapop 10.0 , Gapext 0.5

RLOSDM62

Scoring table:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Detabase :

Published Application (Application Application Applica

Peed. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the rotal score distribution.

STREAMER

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Description	Sequence 69,	Sequence	Sequence	Sequence 623,	Sequence 5	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence 18, Appl
ū	US-10-073-885-69	US-09-895-686-4	US-09-928-175-24	US-10-225-567A-623	US-09-764-853-557	US-09-764-877-2009	US-09-989-442-105	US-09-764-886-52	US-10-073-865-84	US-10-103-313-373	US-10-073-885-96	US-09-928-175-21	US-09-928-175-20	US-10-229-735-3	US-10-321-807-18
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% Query Match Length DB	188	396	757	757	176	176	176	176	176	176	176	718	737	737	355
% Query Match	77.2	77.2	77.2	77.2	76.5	76.5	76.5	76.5	76.5	76.5	76.5	49.5	49.5	49.5	47.5
Score	638	638	638	638	632	632	632	632	632	632	632	409	409	409	392.5
Result No.	-	7	e	7	S	9	۲-	8	6	10	1	12	13	14	15

RESULT 2 US-09-895-686-4

Sequence 13, Appl	Sequence 12, Appl	Sequence 8, Appli	Sequence 6, Appli	Sequence 3, Appli	Sequence 7, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 65, Appl	Sequence 21, Appl	Sequence 4, Appli	Sequence 27, Appl	Sequence 10, Appl	Sequence 3, Appli	Sequence 7, Appli	Sequence 12, Appl	Sequence 6, Appli	Sequence 11, Appl	Sequence 3, Appli	Sequence 2, Appli	Seguence 5, Appli	Sequence 14, Appl	Sequence 6, Appli	Sequence 150, App	Sequence 20, Appl	Sequence 30, Appl	Sequence 13, Appl	
LO US-09-928-175-13	LO US-09-928-175-12	10 US-09-928-175-8	11 US-09-965-536A-6	LO US-09-928-175-3	LO US-09-928-175-7	L1 US-09-965-536A-2	LO US-09-928-175-2	L5 US-10-229-735-1	L5 US-10-222-668-2	11 US-09-930-312-2	L1 US-09-782-974C-66	15 US-10-270-333-21	15 US-10-222-668-4 ·	LS US-10-270-333-27	L1 US-09-965-536A-10	15 US-10-222-668-3	9 US-09-877-804-7	11 US-09-965-536A-12	9 US-09-877-804-6	11 US-09-965-536A-11	9 US-09-877-804-3	9 US-09-877-804-2	9 US-09-862-767A-5	11 US-09-965-536A-14	10 US-09-804-626-6					
949	682	269	713	718	730	737	754	754	754	101	327	334	722	329	1115	1115	675	688	692	692	674	200	458	693	669	669	861	695	687	
47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	42.3	29.5	27.3	27.2	25.7	25.1	25.1	16.9	16.9	16.9	16.9	16.2	16.2	15.9	15.9	15.9	15.9	15.7	15.7	15.6	
392.5	392.5	392.5	392.5	392.5	392.5	392.5	392.5	392.5	392.5	349	244	224.5	224.5	212.5	207.5	207.5	139.5	139.5	139.5	139.5	134	134	131	131	131	131	130	129.5	129	
16	11	18	61	20	21	22	23	24	52	92	27	28	53	30	31	32	33	34	35	36	37	38	39	0.7	41	45	43	44	45	

## ALIGNMENTS

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1 AQIYSVAIPLGINLAARILIVPSYGSKRYSVAQSAITATEIRNOVKKBULAKRFPFIVP 60
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                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 77.2%, Score 638, DB 15; Length 188; Sest Local Similarity 9.18, Pred. No. 2.16-2; Matches 177; Conservative 1; Mismatches 6; Indels 0; Gaps
                                                                                APPLICANT: Rosen et al. TITLE TYTHER PROPERTY NUCLEIC ACIDS, Proteins, and Antibodies FILE REPERFENCE: PAZOSC1
                                                                                                                                                                                           Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 116
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/073,885 CURRENT FILING DATE: 2002-02-14
                 Sequence 69, Application US/10073885; Publication No. US20030096346A1; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                   J ORGANISM: Homo sapiens
US-10-073-885-69
US-10-073-885-69
                                                                                                                                                                                                                                                                                    LENGTH: 188
TYPE: PRT
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"Sequence (21. Application US/0,2257A |
Publication No US200011395A |
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Pred. No. 1.2e-61;
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NUMSHER OF SEQ ID NOS: 939
SOTHWRR: Patentin Ver. 2.0
SEQ ID NO 557
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ilarity 94.0%; Pred. No. 9e-62;
Conservative 1; Mismatches 7; Indels
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CURRENT FILING DATE: 2001-01-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUCREME FILING DATE: 2001-12-19
PRIOR APPLICATION WIMER: 60/27,144
PRIOR FILING DATE: 2006-12-19
NUMBER OF SEQ ID: NOS: 4292
SOFTWARE: PATENTIAN VOS: 4292
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Patent No. US20020090672A1
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Best Local Similarity 94.8%;
Matches 127; Conservative
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US-10-225-567A-623
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ORGANISM: Homo saptens
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Matches 126; Conserva
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LENGTH: 757
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77.24; Score 638; DB 10; Length 757;

Best Local Similarity 94.88; Pred. No. 1.28-61;

Matches 127; Conservative 1; Mismatches 6; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; NAME/KEY: misc_feature
; -OTHER TOTAL TOTAL IN O. US20020106655A1 2488822CD1
S-09-895-686-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 77.2%; Score 638; DB 10;
Best Local Similarity 94.8%; Pred. No. 5.4e-62;
Matches 127; Conservative 1; Mismatches 6;
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CURRENT TILING DATE: 2001-06-28
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PERL, Program
                                                                                                                                                                          NFFICANT: Definition Offs
APPLICANT: All, Preed;
APPLICANT: Tang, Y. Toon
APPLICANT: Baugh, Markah R.
APPLICANT: Baughn, Markah R.
PITER OF INVENTIONS: HUGAN GPOR PROTEINS
PILE REFERENCE: PC-0044 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 24, Application US/09928175
Patent No. US20020123618A1
Sequence 4, Application 05/09895686
Patent No. US20020106655A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              335 WYNTRORKSMDSKG 348
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                                                                                                                                               APPLICANT: Bandman, Olga
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LENGTH: 757
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US-09-928-175-24
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NOL. Negoro, Der. 39, 17155, 195
A. Alfiles Extreduce of the Dovins follole-etimulating hormone receptor complementary
A. Anderessen number 18995, NUTD-55127199; PAINT-7826512
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                   receptor that mediates the blochemical effects of follitropin
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C.Date: 1-04t-1996 *sequence_revision 15-04t-1996 *text_change 21-Jan-2000
C.Accession: 14596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ACTYSVAIFLGINLAAFIIIVESYGSMFYSVHOGAITATBIBNOVKKENTLAKBFFFTVF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2: Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16.9%; Score 139.5; DB 2; Length 695; 26.5%; Pred. No. 3.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60: Indels
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A:Roleorie type: mRNA
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Cigocides: Jatutus norresiona (Knyway Par.)
Cigocomesiona Addisin Aufizia (Knyay Par.)
Cigocomesiona Addisin Aufizia (Knya)
Nol. Benderina, 1. Strann, 7. Mikolice, K. is Sepaloff, D.L.; Seeburg, P.B.
Nol. Endocrina, 4. 532-570, 1990
M. A. Seeburg, P.B. Seeburg, P.B.
M. Seeburg, P.B.
M. Markenene on maber: Addisin WITD-5112538; PWID-5126341 phornone; structure and function Andreasion Addisin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RiLoosfelt, H.; Misrahl, M.; Atger, M.; Salesse, R.; Vu Hai-Luu Thi, M.T.; Jolivet, A.; Science 245, 525-528, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arfitle: Structural organization of the follicle-stimulating hormone receptor gene. A. Reference number: A41729, MOID:92149579; PMID:1738373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AQIYSVAIFLGINLAAFIIIVPSYGSNFYSVHQSAITATEIRNQVKKRMILAKRFFFIVF 50
                                                                                                                                                                                                                                                                                                                                                                                                              C:Species: Sus scrofa domestica (domestic pig)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 21-Jan-2000
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Aimosiduse: 1-65-88-5
AiChoss-references: GB:L02842; NID:g204183; PIDN:AAA41175.1; PID:g204184
                                                                                                                                                                                                                                                                                                           lutropin-choriogonadotropin receptor precursor (splice form A) - pig NyAlternate names: luteinizing hormone-choriogonadotropin receptor
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17.0%, Score 140.5; DB 2; Length 696;
Best Local Similarity 27.3%; Pred. Nb. 2.Be.06
NBtChBs 41; Consorvative 26; Mismanches 55; Indels 29
                                                           HNSHPRNGHCSSAH 576
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Mol. Endocrinol. 6, 70-80, 1992
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C; Function:
540 LLSKFGCYEMQAQIYRTETSSTA--
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A,Molecule type: mRNA
A,Residues: 1-696 <LOO>
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Nationate measu; including phomogeneous consistence of the property of partial measurements of the property of A)Title: Lutropin-choriogonadotropin receptor: an unusual member of the G protein-cou A) Reference number: A41343; MUID: 893372512; PMID: 2507842 A) Accession: A41343. J. Biol. Chem. 264, 4636-4641, 1989 A/fiftle: Purification, characterization, and amino-terminal sequence of rat ovarian r A. Introcens: 58(2): 2072. 2073. 133.72; 13571. 3802. 3802. 332. 332. 3307. 3307. 3307. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 3507. 35 R.MCParland, K.C.; Sprengel, R.; Phillips, H.S.; Koehler, M.; Rosemblit, M.; Nikolios Science 245, 494-499, 1989 Alonesion: Alones number 1, 1984 March 1984 A,Cross-references: GB:M63918; GB:M63919; GB:M63920; GB:M63921; GB:M63922; GB:M63923; Fibrida, M.L.; Misogish, T.; Bucked, S.S.; Deligado, C.J.; Zhang, R. J. Steroid Bicchem, 33, 715-720, 1986 of Gornian and effective Lighted Article Characterization and Structure of Gornian and esticular LEGAG receptors. A: Reference number: A61453, MID: 9090704, PMID: 5601335 528 SQVILSILI-LNVVAFVVICACYIRIYFAVQNPBLTAP-----NRDIKIAKMAILIF 580 61 TDALCWIPI-PVAKPLSLLQVEIPGTITSWVVIGYSAINSALMPILYTLTTRPPKE---- 115 1 AQIYSVAIFLGINLAAFILIVFSYGSMFYSVHQSAITATBIRNQVKKEMILAKRFFFIVF F:153-177/Domain: leucine-rich alpha-2-qlycoprotein repeat homology <LRR> A;Cross-references: GB:N26199: NID:q205178; PIDN:AAA41528.1; PID:q205179 48: Inde1s 12: Length 700; A; Reference number: A32460; MUID: 89174723; PMID: 2925659 16.2%; Score 134; DB 2; 27.2%; Pred. No. 1.3e-05; lutropin-choriogonadotropin receptor precursor - rat A;Status: preliminary A;Molecule type: protein A;Residues: 27-33,'X',35-37,'X',39,'X',41-44 <DUP> 31; Mismatches A;Molecule type: protein A;Residues: 27-32,'LX',35-37 <ROC> Conservative A; Molecule type: DNA A; Residues: 1-700 <KOO> A; Cross-references: GB:M68917 Ouery Match Best Local Similarity 7 R.Roche, P.C.; Ryan, R.J A; Molecule type: DWA A; Residues: 1-320 <TSA> 116 MIRRY 120 541 LLSRF 645 1-700 <MCF> A:Status: preliminary A; Molecule type: mRNA A; Accession: A32460 A; Accession: A61453 A: Residues: C; Genetics: A49744 g à G à Experimental sources overlan expensions on all among according to the G-protein coupled receptors. It has example and coquates to the family of the G-protein coupled receptors. It has example and coquates in female. R:Remy, J.J.; Lahbib-Mansais, Y.; Yerle, M.; Bozon, V.; Couture, L.; Pajot, E.; Grebert, Gene 163, 257-261, 1995 ANTILLE: The portine follitropin receptor: GDNA cloning, functional expressionand chromo A.Reference muker: JC4301; MCID:96011644; PMID:7590277 A.Accession: JC4301 C. Species Nation By C. (Territy C. 1984). Solution of C. Ang. 1986 Float, Chings 21, Jun. 2000
C. Morenton T. 7718 Siller Sequence, Territy C. (Marketorpi, J. T.; Majanieni, R.J.
Man. Lett. Endocriptol. 84, 127, 131, 1352
A. 71111: Expression of the LaWO, Report open in represent of the LaWO, Statement of the LaWO, Sta Albin Postition: 9.0.7-04.

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Sougherfaelly: 9/voprocation homeone receptor; leauther rich alpha-2-9/voprotatin repeat of present companies of profession companies are present as a profession of profe A.introns: 58/2; 82/2; 107/2; 132/2; 157/2; 183/2; 206/2; 231/2; 293/2; 320/2 C.Superfamily: glycoprotein hormone receptor; leucine-rich alpha-2-glycoprotein repeat 526 SOLYVVSL-LVLAVLAFVVICGCYIHIYLIVRNPNIMSS-----SSDTKIBKBABALIF 578 61 TDALCWIPI-FVAKPLSILLQVEIPGTITSWVVIGTSALNSALNPILTTTTFFFFKE--- 115 579 TDELCAVPISFRAISASLKVPLITYSKLKILLVLFYPINSCANPFLYAIFTKNFRRDVFI 638 1 AOITSVAIPLGINLAAFIIIVESYGSMEYSVHOSAITAIBIBNOVKKEMILAKREPEIVE 60 follitropin sceepor - The state of the state 17; Gaps A;Cross-references: GB:S40803; NID:g252163; PIDN:AAB22680.1; PID:g252164 C;Genetics: Score 136.5; DB 2; Length 694; Pred. No. 7.2e-06; Indels 116 MIHRFW-----HNYRORKSMDSKGIRKHMLHHSSGGKCGHC 151 640 LLSKFGCYEVQAQTYRSETSSTA-----HNPHPRNGHC 672 luteinizing hormone/chorionic gonadotropin receptor - rat P.443-464/Domain: transmembrane status predicted cTM3> F19485-507/Domain: transmembrane status predicted cTM4> F208-549/Domain: transmembrane status predicted cTM4> F;573-596/Domain: transmembrane *status predicted <TM6>
F;608-629/Domain: transmembrane *status predicted <TM7> 116 MIHRPWHNYRORKSMDSKGI-RKHMLHHSSGGRCGHC 151 62; 539 LLSKFGCYEMQAQTYRIENLSTAHNIHPRN----GHC A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA A:Residues: 1-700 <RES> 36; Mismatches 16.5%; 42; Conservative A;Cross-references: GB:L31966 Query Match Best Local Similarity A; Molecule type: mRNA A; Residues: 1-694 <REM> A; Accession: 177463 C:Acceston: JC4301 A:Gene: fshr Matches 용 Š g ò g

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: LOCATION: (133)
OTHER INTERMATION: Xea equals any of the naturally occurring L-amino acids 15-10-073-885-96
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Pred. No. 9e-62;
1; Mismatches 7; Indels
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TILE OF INVENTOR: NOCISIC Acids, Froteins, and Antibodies
FILE REBERGE: PJ203C1
             Prior Application removed - See File Wrapper or Palm
SOFTWARE: Patentin Ver. 2.0
SEO 1D NO 373
LENGTH: 176
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CURRENT TELING DATE: 2002-02-14
Prior Application removed - See file Wrapper or Palm
NUMBER OF SRQ ID NOS: 116
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Publication No. US20030096346A1
GENERAL INFORMATION:
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; Sequence 21, Application US/09928175
; Patent No. US2002012361881
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Best Local Similarity 94.0%;
Matches 126; Conservative
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Best Local Similarity
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US-10-073-885-96
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GENERAL IMPORMATION:
APRILCACHER: Rosen et el.
Tring of INVERTION: Riccial Acids, Proteins, and Antibodies
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NUMBER OF SEQ ID NOS: 154
SOFTWARE: PatentIn Ver. 2.0
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CURRENT FILING DATE: 2002-02-14
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Publication No. US20030044904A1
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Publication No. US20030166148A1
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US-10-229-735-3
) Sequence 3. Application US/10229735
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SOFTWARE: PatentIn version 3.1
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PRIOR APPLICATION NUMBER: 50/21.11

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Patent No. 6228597
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REGISTRATION NUMBER: 16773
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TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 56:
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DUMONT, JACQUES
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MEDIUM TYPE: Disk
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ADDRESSEE: CUSHMAN D.
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Sequence 3, Appl
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Sequence 10, Appl
Sequence 10, Appl
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GENERAL INFORMA
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Sequence 55, Appli
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                                                                                                                                                                            September 25, 2003, 14:56:36 ; Search time 30 Seconds (without alignments) 221.427 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 29,
Sequence 54,
Sequence 60,
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826-
1 AQISSVAIPLGINLAAFIII.......HULHESSGGKCGHCRRCHIS 157
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-741-453A-55
US-08-118-20-18
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US-07-757-342D-8
US-07-757-342D-8
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US-08-47-947-3

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US-07-741-4538-64
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US-09-546-117-2
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Result

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POLYPEPTIDES HAVING THIROGROPIN-RECEPTOR
ACTIVITY, UNCLED. ACID SEQUENCES CODING POR SUCH RECEPTORS
AND POLYPEPTIDES, AND APPLICATIONS OF THESE POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                  ATTAMEN OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE DAVID 6. COMLIN: DIKE, BRONSTEIN, ROBEKTS 6.
CUSHMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: IGARASHI, WASAO
MINEGISHI, TAKASHI
NAKAMURA, TAXALCO
INTLE OF INVENTION: PROTEIN, DNA AND USE THERBOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 16.9%; Score 139.5; DB 3; Best Local Similarity 27.3%; Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 31903
REPERENCE/DOCKET NUMBER: 41226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / TOPOLOGY: 11mear MOINGUESTE TOPOLOGY: 11mear MOINGUESTE TYPE: PROFEELD SEQUENCE DESCRIPTION: SEQ ID NO: 6: US-07-557-342D-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 55, Application US/07741453A Patent No. 6228597
                                                                     Sequence 6, Application US/07757342D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
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IENGTH: 692 amino acids
TTPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
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APPLICANT: LIBERT, FREDERIC
APPLICANT: DUMONT, JACQUES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEC ID NO: 6:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VASSART,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02109
                                                                                                                                                  GENERAL INFORMATION:
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RESULT 3
US-07-757-342D-6
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596 SQVEILFILIPIGEOGLAVVARFILICACELKIRFAVQNPELMAT-----NKDFKLAKKM 649
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                                                                                                        56 PPIVPTDALCWIPIPVAKPLSLLQVE----IPGILISWVVIGYSAINSALNPILITL 108
                                                                                                                                                                              550 AVLIPTOPICAAPIGHCGPISPEAISAALKVPLITVTNSKVLLVLFYPVNSCANPFLTAT 709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MUMBER OF ERQUENCES: 10
CORRESPONDEDE ADDRESS: 0.
CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 17.0%; Score 140.5; DB 3; Length 696; Best Local Similarity 27.2%; Pref. No. 5.6e-07; Matches 41; Conservative 26; Mismatches 55; Indels 29; Matches 75; And 20; Matches 26; Mismatches 25; Matches 29; Matches 26; Mismatches 25; Matches 29; Matches 26; Mismatches 26; Matches 26; Mismatches 26; Matches 26; M
                                                                                                                                                                                                                                                    109 TTRPFKEXIHRFWHNYRORKSMDSKGIRKHMIHHSSGGKCGH 150
                                                                                                                                                                                                                                                                                                                         110 PIKAPRR------DPIGHCGFFLLLSKSGCCKH 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MINEGISHI, TAKASHI
NAKAMURA, KAZUCO
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 FWHNYRQRKSMDSKGIRKHMIHHSSGGKCGH 150
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MEDIUM TYPE: FLORPY disk
COMPUTER: IBM PC COMPUTED:
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 4, Application US/07757342D
; Patent No. 6218509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PILING DATE: 10-Sep-1991
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NAME: BUCKLEY, Linds M.
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TELEPAX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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US-07-757-342D-4
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REGORANDO REGO
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FILING DATE: 2000-09-08
APPLICATION NUMBER: 60/229,509
FILING DATE: 2000-09-05
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PRIOR APPLICATION WINDER: 60/234,274
PRIOR FILLING DATE: 2000-09-21
PRIOR FILLING DATE: 2000-09-21
PRIOR FILLING DATE: 2000-09-21
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PRICE APPLICATION WINBER: 60/21, 956
PRICE FILING DATE: 2000-12-08
PRICE FILING DATE: 2000-12-08
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PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,345
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FILING DATE: 2000-07-07
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PRIOR FILING DATE: 2000-08-14
PRIOR FPLICATION NUMBER: 60/251,869
PRIOR FILING DATE: 2000-12-08
PRIOR APPLICATION NUMBER: 60/235,834
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PRIOR FILING DATE: 2000-09-25
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APPLICATION NUMBER: 60/229,513
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FILING DATE: 2000-08-14
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                                                                                                      A AOLYSVALPIGINIA APTRIVESKOSNEY SVHOSALPATETRIONISKEMILA KREPETUF 60
                                                        1 AOIXSVAIPIGINLAAFIIIVESKOSMFYSVHOSAIFATEIRNOVKKEMILAKREPFIVP 60
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THIER DOFT PROPERTION NOTICE AND ADDITIONAL STATE ADDITIONAL CONTRIBUTION NOTICE THE ADDITIONAL TO ADDITIONAL TO ADDITIONAL PROPERTION NOTICE. TO ADDITIONAL TO ADDITIONAL TO ADDITIONAL ADDITION
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TITLE OF INVENTION: Nacleic Acids, Proteins, and Antibodies
FILE PERESEMEN: 9/208
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CURRENT FILING DATE: 2001-11-21
CREADY FILING DATE: 2001-13-31
PRIOR FILING DATE: 2000-01-31
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PRIOR PELINO NUTS. 3000-02-04
PRIOR PELINO NUTS. 3000-02-04
PRIOR PLILAN DEST. 3000-02-04
PRIOR PLILAN DEST. 3000-02-04
PRIOR PELINO NUTS. 3000-06-28
PRIOR PELINO NUTS. 3000-07-11
PRIOR PLILAN DEST. 3000-07-11
PRIOR PLILAN DEST. 3000-07-11
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Patent No. US20020147140A1
GENERAL INFORMATION:
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Publication No. US20030013649Al
GENERAL INFORMATION:
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LOCATION: (133)
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US-09-764-877-2009
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LENGTH: 176
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PRIOR FILING DATE: 2000-11-17

APPLICATION NUMBER: 60/236,367

PRIOR

60/237,040

PRIOR APPLICATION NUMBER: 60/

60/240,960 60/239,935

2000-10-20 PILING DATE: 2000-10-13

FILING DATE: 2000-10 APPLICATION NUMBER: PRIOR APPLICATION NUMBER:

PRIOR PRIOR PRIOR PAPILIZATION PROMESE 66/241.787
PRIOR PILING DATE: 2000-10-30
PRIOR PPLING DATE: 2000-11-08
PRIOR PLING DATE: 2000-11-17
PRIOR PLING DATE: 2000-11-17

PRIOR APPLICATION NUMBER: 60/239,937 PRIOR FILING DATE: 2000-10-13

PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,210 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/226,681 PRIOR FILING DATE: 2000-08-22

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APPLICARE: Roses et al.
TILLS OF PRINKTONS INCLED Acids, Forceins, and Antibodies
TILLS OF PRINKTONS INCLED Acids, Forceins, and Antibodies
TILLS PRESENCE: FIND WORRE: US/OF/OF4.886
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SOFTWARE: PARENTA WEY. 2.0
REGOR PRELOZION (1988): 6 (72.2, 4.0)

REGOR PULLING NURSE: 6 (72.
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Publication No. US20030139327A9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 WYNTRORKSMDSXG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 52
LENGTH: 176
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 8
US-09-764-886-52
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PREOR PILIZARMA 190000 06.47.59
PREOR PILIAN PROPOSO 06.47.59
PREOR PILIAN PROPOSO 06.47.52.213
PREOR PILIAN PRESENCE 3.000-06.42.71.82
PREOR PILIAN PRESENCE 3.000-06.52.71.82
PREOR PILIAN PRESENCE 3.000-06.52.71.82
PREOR PILIAN PRESENCE 3.000-06.52.71.83
PREOR PILIAN PRESENCE 3.000-06.71.83

PRIOR APPLICATION NUMBER: 60/230,438 PRIOR FILING DATE: 2000-09-06 PRIOR PELICATION NUMBER: 60/215,135 PRIOR FILING DATE: 2000-66-30 PRIOR APPLICATION NUMBER: 60/225,266

PRIOR FILING DATE: 2000-08-14

PRODE WILLIAM STATEMENTS (1749, 128

PRODE PILLING DEER, 2000 11, 1749, 1749

PRODE PILLING DEER, 2000 11, 1749

PRODE PILLING DEER, 2000 11,

PRIOR PILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,215
PRIOR FILLING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: 60/249,264

APPLICATION NUMBER: 60/249,214 FILING DATE: 2000-11-17

FILING DATE:

PRIOR PRIOR PRIOR

PRIOR APPLICATION NUMBER: 60/249,297

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Fri Sep 26 08:42:40 2003

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1 AQIYSVAIFLGINLAARIIIVFSYGSNEYSVHQSAITATEIRNQVKKEMILAKREFFIVF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TDALCWIPI-FVAKPLSLLQVEIPGTITSWVIGYSAINSALNPILYTLTTRPFK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 10
CORRESPONDENCES: CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 15.9%; Score 131; DB 3; Length 674; Best Local Similarity 29.6%; Pred. No. 5.8e-06. Matches 34; Conservative 25; Mismatches 48; Indels Matches 34; Conservative 25; Mismatches 48; Indels
                                                                                                                            COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SORTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/757,342D
FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/07/757,342D
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MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: procein
SENGENCE DESCRIPTION: SEQ ID NO: 10:
05-07-73-3420-10
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 41226
                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: BUCKLRY, Linda M.
REGISTRATION NUMBER: 31003
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REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/07757342D
Patent No. 6218509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MINEGISHI, Takashi
NAKAMURA, Kazuto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 130 Water Street
                                                                                                   MEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 674 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617)523-6440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRIEX: 200291 STRE UR
INFORMATION FOR SEC ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: IGARASHI, Masao
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SECURNCE CHARACTERISTICS:
                                            ZIP: 02109
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 02109
                             COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AGIYSVAIFLGINLAAFIIIVFSYGSMFFSVHOSAITATEIRNOVKKEMILAKRFFFIVF 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 TDALCWIPI-FVAKPLSILQVEIPGTITSWVVIGYSAINSALNPILYTLITRPFK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              514 TDFTCARDISFFAISBARKVPLITVTWSKVLLVLVEVPINSCARPFLYALFTKIFO 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
                                                                                                                                                                                                                                                                                                                ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS &
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15.9%; Score 131; DB 3; Length 636; Best Local Shmilarity 29.6%; Pred No. 5.4e-66; Meathes 34; Conscrutive 25; Mismatches 48; Indels Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patchtin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/757,342D
                                                                                                                                                                         MINEGISH, TAKASH
MINEGISH, TAKASH
MINEMIUN: PROTEIN, DNA AND USE THEREOF
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MINEGISHI, Takashi
NAKAMURA, Kazuto
TITLE OF INVENTION: PROTEIN, DNA AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 41226
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TIPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BUCKLEY, Linda M.
REGISTRATION NUMBER: 31003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 10-Sep-1991
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/07757342D
Patent No. 6218509
GENERAL INFORMATION:
                                                                     Sequence 7, Application US/07757342D
Patent No. 6218509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPRONE: (617)523-3400
TELEFRX: (617)523-6440
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                                                                                                                                                                                                                                                                                                                                                                  STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 636 amino acids
TYPE: amino acid
                                                                                                                                                     APPLICANT: IGARASHI, Masao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALTORNEY /AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Massachusetts
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                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02109
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                                                 US-07-757-342D-7
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25 SQLIVMSL-LVLNVLAFVVICGCTHIYLTYRNPNIVSS-----SSDTRIAKRMAMLIF 307
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                                                                                                                                                                                                           305 TDPLCMAPISFRAISASLKYPLITYSKAKILLVLFHPINSCANPFLYAIFTKNFREDFFI 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AQIYSVAIFLGINLAAFIIIVFSYGSMPTSYHOSA1TATEIRNOVKKEMILAKRFFFIVF 60
                                      1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQSAITATEIRNQVKKEMILAKRFFFIVF 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 33, Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 423;
                                                                                                                                                                                                                                                                                                     115 -----EMIHRFWHNYRQRKSMUSKGIRKHMI. HISSGGKCGHC 151
                                                                                                                                                                                                                                                                                                                                                              365 LLSKCGCYENOAOI --- YRTELSSTV----- BNTHPRAGHC 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIILE OF INVENTION: STRAIBGY TO CLONE DRUGS FOR G PROTEIN
IIILE OF INVENTION: COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 -----EMIHREWHNYRQRKSMDSKGIRKHMLHHSSGGKCGHC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  368 LLSKCGCYEMQAQI --- YRTETSSTV -----HNTHPRNGHC 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: NIXON, HARGRAVE, DEVANS & DOILE LLP
: Clinton Square, P.O. Box 1051
Rochester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
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Best Local Similarity 26.1%; Fred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Conservative 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19603/1280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gershengorn, Marvin C.
APPLICANT: Gers-Raaka, Elizabeth
APPLICANT: Nussenzveig, Daniel R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 38, Application US/08795876
Patent No. 6403305
GENERAL INFORMATION:
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ATTORNEY/AREN: INFORMATION:
NAME: SRAMAN, SISMA J. 103
RESTRANCE/OCKET NUMBER: 34, 103
RESTRANCE/OCKET NUMBER: 1560:
FELEDOMENICATION: NUMBER: 1560:
FELEPHONIC: 716-263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 423 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
US-08-795-876-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8: Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TDALCWIPI-FVAXPLSLLQVEIPGTITSWVIGYSAINSALNPILYTHTPFX 114
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15.2%; Score 125.5; DB 4; Length 420;
Best Local Schmilarity 76.18; Pred. No. 1.3e-05;
Matches 43; Conservative 30; Missaches 59; Indels 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: General-Banko, Blizabeth APPLICANT: General-Banko, Blizabeth APPLICANT: General-Banko, Blizabeth APPLICANT: MUNICANTE OF TITLE OF INVENTION: STREAMENT TO LANGE BRUES FOR G PROTEIN WINNERS OF SEQUENCES: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 131; DB 3; Length 699;
29.6%; Pred. No. 6e-06;
Live 25; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP
STREET: Clinton Square, P.O. Box 1051
REFERENCE/DOCKET NUMBER: 41226
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEC ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEOCOMENICATION (TROUGHT)

TELEOCOMENICATION (TROUGHT)

THEIREN, (17) 552-5140

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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33, Application US/08795876
Patent No. 6403305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 716-263-1636
TELEFAX: 716-263-1600
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             420 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 29.68
Matches 34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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MOLECULE TYPE: peptide
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rochester
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                       US-07-757-342D-2
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US-08-795-876-33
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Search completed: September 25, 2003, 15:01:39 Job time: 20 secs

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GenCore	(c) 1993
	Copyright

OM protein - protein search, using sw model

September 25, 2003, 14:55:26; Search time 36 Seconds (Without alignments) 1125:366 Million cell updates/sec Run on:

830525 seqs, 258052604 residues Gapop 10.0 , Gapext 0.5 BLOSUK62 Scoring table: Searched:

Total number of hits satisfying chosen parameters:

830525

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

sp_unclassified:* sp_vertebrate:* sp_organelle:* sp_rvirus:* sp_rodent:* sp_plant: * sp_virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

SUMMARIES

		ep				
Result No.	Score	Query	Ouery Match Length DB :	90	ID	Description
1	224.5	27.2	334	2	09VYG0	O9vvgO drosophila
~	212.5	25.7		'n	09VBP0	O9vho0 drosophila
3	154	18.6		13	09DGC5	Ogdac5 oreochromis
•	148	17.9		'n	095x16	095v16 asterina pe
'n	148	17.9		S	095717	095v17 asterina pe
9	143.5	17.4		13	098785	O98t85 lctalurus p
-	139.5	16.9		Ξ	064183	064183 rattus sp.
00	138	16.7	307	13	090XC7	
6	134	16.2		13	69160	091949 oncorhynchu
10	133.5	16.2		33	Q9DE63	O9de63 rana catesb
11	132	16.0		v	08SPS8	OSSDSS bos taurus
12	132	16.0		Ħ	091948	Q91948 oncorhynchu
13	131			13	Q918N7	0918n7 morone saxa
7	130.5			13	098TF4	098tf4 oreochromis
15	130			'n	Q9BN18	Oppn18 drogophila
16	130			'n	29NKD6	Q9nkd6 drosophila

## ALIGNMENTS

				te)	date)				scta; Pter;	Muscomorph		
	Æ.			npgs	in uo				Inse	era;		
	334 AA.			nence	otati				poda;	achyc	la.	
	PRT;		Created)	Last seq	Last ann			it fly).	oda; Hexa	tera; Br	Drosophi	
			13,	13,	23,			FF	hrope	Dir.	dae;	
	PRELIMINARY		(TrEMBLrel.	(TrEMBLrel.	(TrEMBLrel.	in.		nelanogaster	Setazoa; Art	dopteryqota	Drosophili	1227;
0.5		09vrg0;	01-MAY-2000 (TrEMBLrel. 13, Created)	01-MAY-2000	01-MAR-2003	CG4187 protein.	CG4187.	Drosophila melanogaster (Fruit fly).	Sukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pter;	Neoptera; En	Ephydroidea; Drosophilidae; Drosophila.	NCBI_TaxID=7227;
9716	٥	c)	F4	p+	E4	60	z	s	c)	o	c)	×

SECUENCE PROM N.A. STRAIN-BERKELEY:

Westerniber 2016(0) tendenty 101113;

Addms W.D., Golnkor S. 1., Boll R.A., Boran C.A., Gocoupa J.D., Amanaridae N.C., Sofewar S. 2., 11 D.W., Bolkshins R.A., 2014 R.F., Someward S.A., Someward S.A., Part S.A. 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Següenze R. B., Maria N. D., Kromallar B., Nan K. H., Bolt B.A., The behave S. B., Maria N. D., Kromallar B., Nan K. H., Bolt B.A., The branch S. C., Bogode R., Bonne C., C., Bogode R., Bonne C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WHERE S. CTORDY M.A. Northese B. a paretactorial J. C. GRAPALI K. THEROMORY P. MEROY Y. MERINGER J. S. PROCHAIRS E. SHILL C. J. THEY J. L. SEGRED C. BERRED B. A. CHAIRD J. W. S. OALINER E. B. S. GOLDHAM, APPENDER B. MERCH C. P. ETISE E. I. GOCKHY. H. BETTER N. SCHOOLINER E. B. MEROMET D. ETISE E. I. GOCKHY. H. BETTER N. SCHOOLINER E. MEROMET B. MELDINGER D. R. MEROMET M. ASSOCIATION OF THE MELDINGER STATES AND STATES TO SERVE THE MELDINGER STATES TO SERVE THE MELDINGER STATES TO SERVE THE MELDINGER STATES THE MELDINGER STATES TO SERVE THE MELDINGER STATES THE MENTAL METERS THE MELDINGER STATES THE MELDINGER STATES THE MELDINGER STATES THE METERS THE METERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25.7%; Score 212.5; DB 5; Length 765; 35.9%; Pred: No. 2.2e-13; ive 24; Mismatches 55; Indels 5;
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FREL: ABOOT3553, ARSF6569.0.2; --
FRERses: FEGNO03954; Lgf3.
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Matches 47; Conservative
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WEXIDENTIALISTON, PRABACTORITIS, THE PRINT CAN, GOORDER J. D., ARMAN KD., CHANNER S.E., ROLF, R.M., Druss C.A., GOORDER J. D., ARMAN KD., CHANNER S.E., ARMAN KD., CHANGER S.E., ARMAN KD. S.E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 YSALLFILVNTLSLIFILFSYIRMEQAIRDSGGGMRST----HSGRENVATREAIIVTT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 DALCWIPIFVARPLSLLQVEIPGTITSWV7IGYSAINSALNPILYTLITTRPFKEMIHRFW 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 DCACWLPIIVVKLAALSGCEISPDLYAWEAVEVLPVNSALNPVLYTLTTAAFKQQLRRYC 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 YSVAIFLGINLAAFIIIVFSYGSMFYSVHQS--AITATEIRNQVKKEMILAKREFFIVFF 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h. (51mlarity 27.2s), Score 224.5; DB 5; Length 334, L91mlarity 32.3s, Pred. No. 5.4e-15; Indels 19; Gaps 54; Conservative 27; Mismatches 67; Indels 19; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila salazogadzer (Fruit fly).
Rekaryoza, Merazoa, Krthropoda, Nesapoda; Insecta, Pterygota;
Neoplean, Endopterygta; Diptern, Stachyceta; Maccasurpha;
Bephrocieles, Drosophilidae; brosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 HNY------RORKSMDSKGIRKHMLHHSS--GGRCGHCRRCH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    282 HILPSCSLVNNETRSQTQTAYESGLSVSLAHLGGGVGGSSGRKRASH 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFASE PROTODI) TYTALI 1 1.
PROSTURS, PROTOSI OF PROTERN RECREPE 1.2; 1.
PROSTUR, PROSTOR SECREPE 1.2; 1.
PROSTURS, PROSTOR SECREPE 1.2; 1.
PROSTURS, PROSTOR SECREPE 1.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FlyBase; FBgn0030458; CG4187.
InterPro; IPR000276; GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001901; SecE.
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01-MAX-2003 (TrEMBLrel.
01-MAX-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 54; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N.A.
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5; Gaps

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719 AKVY-VGSILILMILAFVIIMACYASIYLAIOGSHAWNCNDSR------VARRMSLLV 769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         770 FIDFACWAPIAFPSLIAAFGLRLISIDGAKVLFIFVL----PLNSCANPFLYTILIKOFK 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ACIYSVAIFLGINLAAFILIVFSYGSMFYSVHOS-AITATEIRNOVKKEMILAKRFFFIV
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- - SUBCELLULAR LOCATION: INTEREAR MERREARE PROFIEIN (ST SMILARITY).
- - SIMILARITY: BELONGS TO PAKILY 10F G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
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"CDN cloning and functional analysis of a novel, member of the
slycoptoctain hormone receptor family from a startish Asterian
glycoprotein hormone receptor family from a starfish Asterina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17.9%; Score 148; DB 5; Length 1012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eleutherozoa; Asterozoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asterina pectunisma (starfish).
Rukaryoti, Metazos, Echinodemata; Bleutherozos; Asterioso
Rukaryotis, Matazosa; Palvatida; Asterinia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               826 KDCKTIMRSLSNRVFROR-SN-SRSITLSLGRHPS 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1.3e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
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SWART: SM(0015; IRRNY; 1.
PROSTR, PS00253; G.PROPER, RECEP_F1_1, 1.
PROSTR; PS00263; G.PROPER, RESPE_F1_2; 1.
PROSTR; PS00263; G.RR, TYPICAL; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-DEC-2001 (TrEMBirel. 19, created)
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00237; GPCRRHODOPSN.
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Matches 51; Conserva
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                                   ectinifera.";
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                            63 ALCHIPIFVAKPLSILQVEIPGTITSNVVIGYSAINSALNPILYTLTTRPFKEMIH-RFW 121
                                                                                                   561 FICWVPIIVMKIWVFFNYNISDDIYAMLVVFVLPRINSAVNPILFYTFYTFRYRDKYRNOIPLRGW 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Openoficonis miloticus (Mile tilapia) (Tilapia milotica).
SMEARYON: Metrazos (Inductatis (Enalatas Vertebruta (Butaleostemi) Actinopterygli, Neopterygli, Telestei Butaleostei (Meoriaestei) Acanthomeryaia, Acanthoperygli, Percomorpha: Perciformes; labroidei: Cichliddes Opecohronis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEGURETO FROM N. A. TO DATE FROM N. TO DATE AND THE ALTHOUGH TO THE ALTHOUGH THE ALT
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"CDNA cloning and functional analysis of a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13: Length 693;
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Bukaryota, Metazoa, Rohinodemata, Eleutherozoa, Asterozoa;
Asteroidea, Valvatacea, Valvatida, Asterinidae, Asterina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44: Indels
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01-WAR-2001 (TrEMBLzel. 16, East sequence update)
01-WAR-2003 (TrEMBLzel. 23, Last annotation update)
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01-DEC-2001 (TTEMBLE1. 19, Last sequence update)
01-MAR-2003 (TTEMBLE1. 23, Last unnotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            693 AA.
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APGFHR'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gonadotropin receptor II.
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                                                                                                                                                                           122 HNYRORKSMDS 132
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY:
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                                                                                                                                                                                                                                                  721 KKITSRKBARA 731
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Matches 40; Commerce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID-8128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Q95Y16
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522 SQLXVMAL-LVLNULAFVVICGCYTHIYLTVRNPTIVSS-----SSDTKIAKRMATLIF 574
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       575 TOPLCMAPISFFAISASLKVPLITVSKAKILLVLFTPINSCANPFLFAIFTKNFRDFFI 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | Webs. | Webs
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                                                                                                                                                                                                                                                                                                                             Bukaryota; Metacoa; Chordata; Craniata; Vertebrata; Butaleostomi;
Mammalia; Extheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NEB_CARID=10118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heckert E.L., Daley I.J., Griswold M.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 MIHRF------MHNTRQRKSMDSKGIRKH------MIHHSS 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            635 ILSKPCCYENQAQIYRTETSSATHNFHARKSHCSSAPRVTNSTVLVPLNHSS 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alkaryota, Metrzoa, Chordata, Craniata, Vertebrata; Euteleostoal;
Actinopterydi; Meopterydi; Teleostel; Enteleoste;
Protazontopterydi; Salmoniformes; Salmonidae; Salmo.
NSE_TextD=8030;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 11, Length 688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-026'-2001 (TREMERICAL 19, Created)
01-026'-2001 (TREMERICAL 19, Last sequence update)
01-MAR-2003 (TREMERICAL 23, Last annotation update)
01-MAR-2003 (TREMERICAL 23, Last annotation update)
Salzo salar (Atlantic calano).
                                             064183.
064183.
064183.
064183.
064189.
064189.
06409.1996 (TERBELLEL 0), Created,
01-8094.1996 (TERBELLEL 0), Last sequence update)
01-8094.1996 (TERBELLEL 0). Last sequence update)
POLICIA estimalating hormone tocopico.
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1 Similarity 27.3%; Pred. No. 6.8e-06;
47; Conservative 30; Mismatches 60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-92149579; PubMed-1738373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00001; 7tm_1; 1.
Pfam; PF00560; CRR; 3.
Pfam; PF01462; ERRNT; 1.
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Best Local Similarity
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090xc7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TDALCHIPI-FVARPLSLLQVEIPGFITSWVIGYSAINSALNPILYTLTFRPRE---- 115
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                                                                                                                                                                                                                                                                                                                                                                                                                       719 AKYY-VGSILILMILAFVIIMACYASIYLAIOGSHAWMCNDSR-----VARRMSLLY 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 FIDALCWIPI----FVAKPLSLLQVEIPGTITSWVIGYSAINSALNPILYTLFTRPFK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            770 FIDFACMAPIAFFSLIAMFGLELISLDGAKVLTIFVL---PLMSCANPFLFTILIKOFK 825
                                                                                                                                                                                                                                                                                                                             1 AQIYSVAIFLGINLAAFIIIVFSYGSMFYSVHQS-ALTATBIRNQVKKEMILAKRFFFIV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wellichkeuligist, benderlandigist, in Treit, i
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ches 66; Indels 21; Gaps
                                                                                                                                                                                                                                           Gaps
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Actinoptezyota; Neopterydii; Teleostel; Ostariophysi; Siluriformes;
Irchiurdes; Icasimuss
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                                                                                                                                                Length 1280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 MIHREWHNTRORKSMDSKGI-----RKHMLH--HSSGGKCGHCR 152
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                                                                                                                                                                                                                                  51: Indels
G-protein coupled receptor; Receptor; Transmembrane.
SEGUENCE 1280 AA: 141700 MW: 0AB0ECCC0DD880BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 696 AA; 77822 NW; 4AIFB19CDE070AB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TEXHBLREL. 17, Created)
01-JUN-2001 (TEXHBLREL. 17, Last sequence update)
01-MAR-2003 (TEXHBLREL. 34, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      826 KDCKTIMKSLSNRVPRQR-SM-SKSITLSLGRHPS 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 ---EMIHREWHW--YRORKSNDSKGIRKHMLHHSS 144
                                                                                                                                                17.9%; Score 148; DB 5;
32.9%; Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             696 AA.
                                                                                                                                                                                                                                  27; Mismatches
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29.5%; Pred. No. 2.6e
Live 30; Mismatches
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Matches 49, Conservative
                                                                                                                                                                                              Best Local Similarity 32.98
Matches 51; Conservative
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                                                                                                                                                Query Match
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this SWIEST-SPOT entry is copyright. It is produced through a collaboration between the SWIES Institute of Bioinformatics and the EMBL outstation. The Burgean Bioinformatics institute, There are no restrictions on its lush by non-profit institutions as long as its content is in no way
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Migrature-301317; Mondey-314442,
A Straw Mr., Solow-Grow P. St. invitor getton and potential control
A Garran Mr., Solow-Grow P. St. invitor getton and potential control
A Garran Mr., Solow-Grow P. St. invitor getton and potential control
Mr., Report of the Overa Foliatropia, neepton gene. Pro. Invitor Control
Mr., Special Control Foliatropia Processis which setting
A Land Mr. octans. St. Strong PSTR 50 of STR 151 and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babu P. M., Jang L., Salram A.M., Touye R.M., Sairam M.R.; Jang L., Salram A.W., Sairam G. V., Sarbina J., Sarbina J.M., Sarbina J., Sarbi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      follitropin receptor with selective alteration in the carboxy terminus that effects standarding function."

Nol. Reprof. Dev. 48:458-470(1997).
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"Confuse of alternete's paicled mank transcripts coding for variants
of owite testicals follitropin receptor lacking the o protein
complied quantits".
Hooping. See. Commun. 190:888-884(1993).
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SIMILARITY: BRIONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPPORS.
                                                                                                                                                                                                                                                                                                                                                           Molecular cloning and expression of the ovine testicular follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Molecular cloning, structure, and expression of a testicular
                                                                                                                                                                                                                                                                      Farney T.A., Sairam M.R., Khan H., Ravindranath N., Payne S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zarney T.A., Jiang L., Khan H., MacDonald B.A., Laird D.W., Sairam M.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ŠEĞUENCE FROM N.A. (ISOFORM FSH-R2), AND CHARACTERIZATION.
SETRAIN-DOSEEL-LAGESTE-TRIFFICH, 1; TISSUE-TESTIE;
SETRAIN-DOSEEL-LAGESTE-TRIFFICH PROPERTY PROPERTY PROPERTY OF THE STATE OF THE SET OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM FSH-R3), AND CHRRACTERIZATION.
STRAIN-HOUSEL Left-Gester-SHIFGLA 1; TISSUB-OVALY;
REDIXING-ZOS912S; PubMed-1027886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FSH/LSH/TSH SUBFAMILY.
SIMILARITY: Contains 6 leucine-rich (LRR) repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-DOYSet-Ledoester-Suffolk 1, TISSUE-Testis;
MEDLINE-93176195; pubMed-8439338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECURICE FROM N.A. (ISOFORMS FSH-R4 AND PSH-R3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                601, Cell Biol. Res. Commun. 2:21-27(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                             stimulating hormone receptor. "; 
Wol. Cell. Endocrinol, 93:219-226(1993).
                                                                                                                                       SECURNCE FROM N.A. (ISOFORM FSH-R1).
                                                                                                                                                                                                                            MEDLINE-93351750; PubMed-8394255;
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        Sovidae, Capringe, Ovis
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                                                           NCBI_TaxID-9940;
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                                                                                                                                                                                 TISSUE-Testis:
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        993 TDECCMVPIIVIGFVSLAGARADDOVYAWIAVFVLPLASAINPVIYTESTAPFIGNVSKR 1052
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197539; G23273; G23273; G23574; G95258;
10.7001-1494 (Rel. 12. Created)
10.7001-1494 (Rel. 12. Last amosturo update)
19.7001-1994 (Rel. 12. Last amosturo update)
19.7001
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Wakaryota, Metacoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mamania; Mitheria; Cetartiodactyla; Numinania; Pecora; Bovoidea;
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
      Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Missing (in isoform PSH-R4).
/FTIG=VSP_001956.
DISFTRIESTRSUBSYGLENLKKLRAKSTYHLKKLPSLE -> S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LISNIGIK -> FKRWENEI (in isoform FSH-R4).
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CHHESSLEVARGNIFLALD (in 1soform FSH-R2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Phosphorylation; Repeat; Lectine-rich repeat; Alternative splicing. PROSSNA. 1 17 nowwww.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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SEMENT SENDORSTANDARDOBSN.
SEMENT SENDORSTALLER.
FORDSTEEN SENDORSTALLER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Missing (in isoform FSH-R2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 (POTENTIAL).
EXTRACELULAR (POTENTIAL).
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1 (POTENTIAL).
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FBF75D89D88C0D4B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL).
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/FTId=VSP_001957.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /FT1d-VSP_001959.
      modified and this statement is not removed.
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ISSP: P23445; IUNA.
InterPro: IRPRODATO'S PERCENCED IN INTERPREDIATE INTERPREDIATE IN INTERPREDIATE INTERPR
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LRR 4.
LRR 5.
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                                                                                                                                                         112766; AAA31523.1; -. 112767; AAA31524.1; -. 136115; AAK70667.1; -.
                                                                                                                                EMBL; L07302; AAA31525.1; -.
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This striss form early is opergright. It is produced though a collaboration between the Suss institute of Bioinformation and the Bing contraction. The Engages and indifformation institute. Pages are no restrictions on its use. Par non-profit institute and make the same by the profit institutions as noney at lease when the commercial entities allowed an agenesal (see http://www.isb-sh/chonomow/or send on sent) to license(abs-sh/oh).
61 TDALCWIPI-FVAKPLSELQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKE--- 115
                                                                                   SEO TDELCHAPISFFAISBSLKVPLITVSKSKILLNLFTPINSCAMPFLYALFTRNFREDFFI 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROBABLE GLYCOPROTEIN HORMONE G-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last septece update)
20-ZUR-2094 (Rel. 41, Last annotation update)
Probable glycoprotein hommone G-protein coupled receptor precursor.
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-i- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROFEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pidan PROPOSIT EML. Tr.
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Mikaryota, Metzoa, Chifaria, abritozoa; Zoantharia; Actiniaria;
Nynantheas, Actinidae; Anthoplaura.
                                                                                                                                                                              116 MIHRFW-----HNTRORKSMDSKGIRKHMLHHSSGGKCGHC 151
                                                                                                                                                                                                                                                         540 LLSKPGCYEVOAOTYRSETSFTA-----HNFHPRNGHC 672
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CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT: 925 AA.
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PIR; JC2033; JC2033.
InterPro; IPR000276; GPCR_Rhodpsn.
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Troplasmic (Potential)

DOMAIN

1 AOTYSVAIFLGINIAAFIIIVFSYGSMFYSVHOSAIFATEIRNOVKKEMILAKRFFFIVF 60

/ Match 17.4%, Score 143.5; DB 1; Length 695; Local Similarity 27.2%; Pred. No. 7.7e-06;

32; Mismatches

Conservative

445

Matches

à

Query Match

59; Indels 27; Caps

us-10-049-568-2,rsp

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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 TDFLONAPISFRAISASLKVPLITVSKAKILLVLFYPINSCANPFLYAIFTRNFRRDFFI 639
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01-402-1940 (Rel. 15, Last sequence update)
01-407-1940 (Rel. 15, Last sequence update)
14-760-1940 (Rel. 15, Last sequence update)
14-760-1940 (Rel. 14, Letter annotation update)
14-760-1940 (Rel. 14, Letter)
                                                                                                                                                                                                                                       FRIEDS, PRODEZI, CACHRENDODEN.
SMART, SMOOLSI, LARRIT, CACRE, FILL, 1.
REGISTE, SOUGSI, LARRIT, CACRE, FILL, 1.
REGISTE, SOUGSI, CARRITLARGER, FILL, 2.
1. CACRETE, SOUGSI, CARRITLARGER, FILL, 2.
1. CACRETE, SOUGSI, CARRITLARGER, T., 2.
1. CACRETE, SOUGSI, CARRITLARGER, T., 2.
1. CACRETE, SOUGSI, CARRITLARGER, SIGNAL, SIGNAL, SIGNAL, STANDARGER, CALVORTOTERI, SIGNAL, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.

**INKED (GICNAC...) (POTENTIAL).

**N-LINKED (GICNAC...) (POTENTIAL).

**N-LINKED (GICNAC...) (POTENTIAL).

**INKED (GICNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.1%; Score 141.5; DB 1; Length 695; 26.5%; Pred, No. 1.2e-05; ive 32; Mismatches 63; Indels 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116 MIHRPW-----HNYRORKSMDSKGIRKHNLHHSSGGKCGHCRRCH 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      640 LLSKFGCYEMQAQIYRTETSSTA-----HNSHPRNGHCSSAH 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                            Phosphorylation, Repeat; Leucine-rich repeat.
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                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
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LRR 4.
LRR 5.
LRR 6.
                                                                             PER, JN00898; JN0898; LRSP, P23945; LXUN.
INCELPEO; IPRO00276; GPCR_Rhodpsn.
InterPro; IPRO0161; LRR.
InterPro; IPRO00372; LRR_Nterm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    78343 MW:
                                      EMBL: X74454; CAA52463.1; -. PIR; JN0898; JN0898.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44; Conservative
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                                                                                                                                                                                 Pfam; PF00001; 7tm 1; 1.
                                                                                                                                                                                                                        Pfam: PF01462: LRRNT: 1
                                                                                                                                                                                                     Pfam; PF00560; LRR; 3.
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318
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TRANSMEM
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CARBOHYD
CARBOHYD
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1D P1651
DT 01-N
DT 28-P
DE 14th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    694 VAFILLVNGASFISVMYLYSRMLYVV----VSGGDARGAPKRADSKVAKRAAILVFTDAL 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-1933 (Rel. 27, Created)
01-0CT-1933 (Rel. 27, Created)
01-0CT-1933 (Rel. 27, Last sequence update)
92-FES-2033 (Rel. 4J, Last annotation update)
F0llicle stimulating hormone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARIET: BELONGS TO FAMÍLY 1 OF G-PROTEIN COUPLED RECEPTORS. FSH/LSH/TSH SUBPAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          control 1, the Marker B. (Shram 8.5, stateshing at the Walterlan Clothing of the testicular Collicie etimatating bornoon expect of the now human primare Means facelinaris and shockers at the Marker State Means the Colliniaris and the Marker State State
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Enkaryota, Netrazon, Inchedita, Craniata, Vertebrata Enteleosromi,
Mammalia, Butheria, Primates, Catarrini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 CWIPI-FVAKPLSLLQVEIPGTITSWVVIGYSAINSALNPILTTLTTRPFK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 750 CWAPIAFFGLLAAFGQTLLTVTOSKILLVFFFFINSICNPFLYAFFTKAFK 800
                                                                                                                   7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
5 X APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 925;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          47; Indels
                                                                                                                                                                                                                                                                                                                                                                                      (in isoform Short).
                   EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         MW; D03A256368452FBD CRC64;
                                                                                                    EXTRACELLULAR (POTENTIAL)
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                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADENTLATE CYCLASE.
                                                                                                                                                                                                                                                           S (INCOMPLETE).
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 143; DB 1;
Pred. No. 1.2e-05;
                                                                                                                                                                                     (INCOMPLETE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Mismatches
   CPOPENTAL.
                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE-94071854; PubMed-7504463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                         925 AA: 100059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID-9541;
                                                                                                                                                                                                                                                                                                                         435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 37: Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEGUENCE FROM N.A.
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                   DOMAIN
                                                         DOMAIN
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FRANSMEN
                                                                                                                   PRANSMEN
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                                                                                                    NIAMO
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                                                                                                                                                                                                                                               RPEAT
                                                                                                                                                                                 REPRAT
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FSHR MACEA
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10000
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This STRESSORY marty is copyright. It is produced through a collaboration between the State factures of Boinformation and the State contraction the buryone bother markets of markets and the State contraction to the buryone bother markets of markets and the statement is not removed. Using the part of commercial markets allowed symptoms of the statement is not removed. Using by and for commercial markets allowed symptoms of the statement of the s
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Science 245-25-254 (1991)

Science 255-254 (1991)

Science
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ISOIG-P16582-4; Sequence-VSP_001967;
SIMILANTY: BILONGS TO FMILLY I OF G-PROFEIN COUPLED RECEPTORS.
PSH/ISH/TSH SUBFAMILY
                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                              SEQUENCE PROM N.A. (ISOPORNG A. B. C AND D).
MENDALWES-BASISTIF PROBLES-STOREM, SALESSE R., Thi M.T.V.H.-L.,
LOOSFEL H., Mischil M., Arger K., Salesse R., Thi M.T.V.H.-L.,
OGIVER, A., Guicchon-Mentel A., Sar S., Jallal B., Garnier J.,
Milgrom E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId-P16582-2; Sequence-VSP_001963, VSP_001964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=C;
Isold=Pl6582-3; Sequence=VSP_001965; VSP_001966;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- SIMILARITY: Contains 6 leucine-rich (IRR) repeats.
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2 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event-Alternative splicing; Named isoforms-4;
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CYTOPLASMIC ()
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name-A;
IsoId-P16582-1; Sequence-Displayed;
(LSH-R) (Luteinizing hormone receptor).
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Radio, 199223, MAJJOGA 11.
Radio, 199227, Radio, 19922
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505
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547
                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                       Sus scrofa (Pig).
                                                                                                                                                                                                       NCBI TaxID-9823:
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## GenCore Version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues Searched: 127863

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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This SHISS PROT entry is copyright. It is produced through a collaboration between the Dayles institute of Bioinformatics and the Real outstatum the Runcess institute of Bioinformatics and the Surcess of Bioinformatics institutes. There are no restrictions on its burges by non-profit institutions as long as its concern is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Makaryota, Merazoa, Chordata, Craniata; Vertebrata, Buteleostomi; Mommalia; Detheria; Modentia; Schurognathi; Murides; Muxinae; Mus
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PROSITE: PS01209; LDLRA_1; 1.
PROSITE: PS50068; LDLRA_2; 1.
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THE RECEIVENING CLASS R 1.

THE RECEIVE CLASS R 1.
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HSSP; 007954; 1CR8.
Interpro; IPR000276; GPCR_Rhodpsn.
Interpro; IPR0002172; LDL_receptor_A.
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D (GLCNAC. .) (POTENTIAL).
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I TISSUES SEPERITIFY: PROMISERABLY MEMORIS SYSTEM AND TO A LESSER EXTERN WEDGENER WITHIN THE CENTRAL MEMORIS SYSTEM AND TO A LESSER EXTERN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D->Y: LEADS TO CONSTITUTIVE INCREASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.5%; Score 392.5; DB 1; Length 754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2088ECD204C6A6C5 CRC64;
                                                                                                                                                                                                                                                                                              (GLCNAC. . . ) (GLCNAC. . . )
                                                                                                                                                                                                                                              BY SIMILARITY.
N-LINKED (GLONG. . .)
N-LINKED (GLONG. . .)
N-LINKED (GLONG. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG-VAR_015386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTIG=VAR_015387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            No. 8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT: 1115 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 59.1%; Pred. No. 8e-2
75; Conservative 25; Mismatches
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inactive).
                                                                                                                                                                                                                                                                                                                                         N-LINKED
N-LINKED
ERR 20.7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86452 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     754 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEOUBNCE FROM N.A.
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P45023;
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284 KMSLVIVLTFIVCWTPYYLLGIWYWFSPEMLTSRKVPPSL-SHILFLFGLFWTCLDPIIY 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 GLFTIHFRRIRRVCRCATOGKDADATSLGTGSFRISTAAVPLKRSAGASGGSCKFDLEV 402
                                                                         TOALCHIPT-PVAKPLSLIOVRIPSTITSHVVIGYSAINSALNPIEXTLTRPEK---- 114
                                                                                                                                                                                                                                                                                                              677 IDELCNAPISFYAMSAVLDRPLITVSNSKILLVLFYPLNSCANPFLYAIFTKAFRGDVFI 736
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1 ACIYSVAIFIGINLAAFIIIVPSYGSMPYSVHQSAITATRIRNQVKKEMILAKRPPFIVF 60
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUP-Brain;
WEDLIRE-DISS, PubMed-11120886;
WARD L. BOSERG J., Chol H.S., Seong J.Y., Soh J.M., Chun S.Y.,
Ward L., Bogerd J., Chol H.S., Seong J.Y., TG M.H., BCChun S.N.,
Highenrohr M., Troskie B.E., Millar R.P., TG M.H., BCChun S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REDIAND-21407809; PubMed-11517181;
Mang L., Oh D.Y., Bogerd J., Chol H.S., Ahn R.S., Seong J.Y.,
Wang H., Oh D.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kwon H.B.; "Three distinct types of GnRH receptor characterized in the
                                                                                                                                                                                                                                                                                                                                                                                                                                 115 -----EMIHRFWHNYRORKSMDSKGIRKHMLHHSSGGKCGHCRR 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               737 LISKWCLCORRADIER-GOTVSSKG-----SSGVCHOGRR 770
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01-MR-2001 (TERBLEE] 16, Last sequence update)
01-DR-2001 (TERBLEE]. 19, Last annotation update)
GRH receptor-3 (Type II GRHR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 98:361-366(2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168 IDFLCMAPISFYAMSPWVDRPL----ITVSNSKILLVLFYPLNSCANPFLYAIFTKAF 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AQIYSVAIPLGINLAAFIIIVFSYGSMFYSVHOSAITATEIRNOVKKEMILAKRFFFIVF 60
                                                                                              *** Table 1.** The set in the control of Atlanto ealed on contra thyrotopin respect (STRE) like control of Atlanto ealed on one tan thyrotopin respect (STRE) like control of Atlanto ealed on the State of Carlon of State of Carlon of State of Carlon of Carlon of State of Carlon of Carlo
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PROGIER, PSOJOZI, CLPROTERN.BOCRE_FILI; I.
G-PROCEIR DOBLOG ROCEPORE, RECEPELOR, TRANSMEMBLAND.
STROMBER SIL AM, SIJOI MM; IRVSAARBOGGSILE CROC6;
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28.9%; Pred. No. 4.1e-06;
14ve 25; Mismatches 41;
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PETRAIS PRODOSO, LURE, 1.

PRINTS: PRODOSO, LURE, 1.

PROMOTER, PRODOSO, 1.

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PROSTER, PSE0237, G_PROTEIN_RECEP_F1_1; 1.
PROSTIE; PSE0263; G_PROTEIN_RECEP_F1_2; 1.
RECEPFOR, Signal.
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Within S. Haus S.Y., Steach N.J.; Genciae-rich repent-containing 6
Characterization of two fly LDR (Leucine-rich repent-containing 6
Profestro-contained reseptor) profests handshopus to variethree
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Ramyota, Necasos (Gondens, Constata, Vetreberba Pieteleostoni;
Actinopersysti: Neoprerysji: Teleoste; Esteleostes;
Actinopersysti: Neoprerysji: Teleostes; Esteleostes; Neoteleostes;
Caralhosorpha, Asanthoppersysi; Percomorpha; Perciformes; Labroide;;
Ciolildes, Orgodoronis;
641 TDFLCMAPISFYAMSAVLDRPLITVSNSKILLIVLFTPLNSCANPFLYALFTKAFR 695
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Bakaryot Methodos Arthbooda Esespola; Insecta; Pterygota;
Rospeta; Endergryger; Dipera Erasolyear; Misconorpha;
Ephydodas; Drosophilidae; Drosophila.
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01-JUN-2001 (TERMEIREL. 17, Inst Sequence update)
01-MAR-2003 (TERMEIREL. 23, Last annotation update)
Leuchne-rich repeat-containing 6 protein-couplast seeptor 2.
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PROSTINE, PROJECT, C., EMPOREM, REZER, T., 1.

PROSTINE, PROJECT, C., EMPOREM, REZER, T., 1.

"SPROSTES, PROJECT, C., PROFEREM, RECREPELT, 1.

"SENDINEME." THE PART, PT. 15 MM. G., 1813.14295880.ABS CRC64,
                                                                                                                                                                                                                                                                                                   1.9 AA.
01.500.7001 (TERRETAL 17, Created)
01.4004.5001 (TERRETAL 17, Last anotation update)
17 Myrotropia receptor.
1758-R. pia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.8%; Score 130.5; DB 1
28.0%; Pred. No. 6.5e-05;
                                                                                                                                                                                                                                                                                         778 AA
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                                                                                                                                                                                                                                                                                         PRELIMINARY:
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Pfam; PF00560; LRR; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WCBI TaxID-8128;
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                                                                                                                                                                            RESULT 14
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704 ASLIYVISLMFINGCAPLILMGCYLKMFWAIRGSQAWWT-----NDSRIAKRMALLVF 756
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 1050;
(1) 4GD 100 too LECT to tronsfered mammalian colls ", sharited (100-200) to the EMEL/CHOST databases EMEL AFFACTS, AMELINES OF THE EMEL AFFACTS, TATABASES, TATABASES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1050 A&: 117707 MW: 35D71260A8B4BF99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15.7%; Score 130; DB 5; 30.9%; Pred. No. 0.0001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PSS0262; G PROTEIN RECEP PL 2; 1.
PROSITE; PS50506; LRR_IYPICAL; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: September 25, 2003, 15:00:38
Job time: 38 secs
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Natches 38; Conserv
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while SHRESPORT entry its opportunit. It is protected through a collaboration between the Shise Institute of Hishinformation and the Diffu contraction the Baropean individual mentione. There are no restrictions on its was no profess to manufacture as not so that is not provided in the property of the 
                        61 TDALCWIPI-PVAKPISLIQVEIPGTITSWVVIGYSAINSALNPILYTLTTRPFKE---- 115
                                                      - PUNCTION: RECEPTOR FOR FOLLICLE STANDLATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
8-FBP-2003 (Rel. 4), Last annotation update)
POllicle atimilating hommone receptor precursor (FSH-R) (Follitropin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Boude A., Lambert A., Sammarde J., Silversides D.N., Lussier J.G.; Structure of the Dovine follicie-stimilating hormone receptor complementary DNA and expression in bovine tissues."; DNA. Reprod. Dev. 39:127-133(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     - SUPCELTULAR COCATION: Integral membrane protein.
STRILARITE SERIORS FORMILY.
PSEJ/LARITES SUBPRILY.
- SIMILARITE: Contains 6 leucine-rich (IRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLITICIE STIMULATING HORMONE RECEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metzzas, Chordata; Craniata; Vertebrata; Butaleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Perora; Bovoídea; Bovídae; Bos,
                                                                                                                            115 MIHRF-----MHNYRORKSMDSKGIRKH-----MLHHSS 144
                                                                                                                                                                    639 ILSKRGCIEMQAQIYRTETSSATHNFHARKSHCSSAPRVTNSYVLVPINHSS 690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSTIE; PS00237; G_PROTEIN_RECEP_E1_1; 1.

PROSTIE; PS00237; G_PROTEIN_RECEP_E2_1.

G-protein coupled receptor: Transmembrane (Bycoprotein; Signal); PROSPIO:YAlation; Repeat; Leucine-rich repeat.
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                                                                                                                                                                                                                                                                                                          695 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Holstein; TISSUE-Ovary, and Testis;
MEDLINE-95127199; PubMed-7826612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR_Nterm.
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SMART; SM00013; LRRNT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 122319; AAC37324.1; -.
                                                                                                                                                                                                                                                                                                          STANDARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00001; 7tm_1;
Pfam; PF00560; LRR; 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR, 145896; 145896.
HSSP; P23945; 1XUN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID-9913;
                                                                                                                                                                                                                                                                                      P35376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor).
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DOMAIN
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                                                                                                                                                                                                                                                        RESULT 10
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                        Heckert L.L., Daley I.J., Griswold M.D., Structural organization of the follicle-stimulating hormone receptor
                                                                                                                            FUNCTION: RECEPTOR FOR FOLLICLE STINGLATING HORMONE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY G PROTEINS WHICH ACTIVATE
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                                                                                                                                                                                                       -i- SUBCELIMIAR LOCATION: Integral membrane protein.
- TISOUS PROTEINTINY: SERVINI CERLE, ANNO VANRIAN GRANULOSA CELLES.
- SIMILARIY: BELONGS TO FAMILY 10F G-PROTEIN COUPLED RESEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOLLICLE STIMULATING HORMONE RECEPTOR.
EXTRACELLULAR (POTENTIAL).
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(GLONAC. .) (POTENTIAL).
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2 (POTENTIAL).
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N-LINKED (GLONAC..
N-LINKED (GLONAC..
N-LINKED (GLONAC...
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InterPro; IPR001611; LRR.
InterPro; IPR000372; LRR. Mterm.
MEDLINE-92149579; PubMed-1738373;
                                                                                                        Endocrinol, 6:70-80(1992).
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HSSP; P23945; 1XUN.
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modified and this statement is not removed. entitles requires a license agreement (See ) or send an email to license@isb-sib.ch).
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Pfam; PP00560; IRR; 2.
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This SMCS-form earry is operight, it; produced through a collaboration between the Suiss institute of Eichichmanics and the ERRA contraction — the Burgean ablichformatic institute. There are no exercitions on its when by non-proofit institutions as long as its content is in no way in no pay.
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Mammalla, Butheria, Primates, Platyrrhini, Callitrichidae.
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15-UL-1998 (Rel. 36, Last sequence update)
18-TW-2003 (Rel. 41, Last aimotetion update)
18-TW-2003 (Rel. 41, Last aimotetion update)
18-TW-2003 (Rel. 41, Last aimotetion update)
18-TW-2004 (Rel. 41, Last aimotetion update)
18-TW-2004 (Rel. 41, Last aimotetion update)
18-TW-2004 (Lastialistic physioletion)
18-TW-2004 (Lastialistic physiol
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Pred. No. 1.8e-05;
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                                                       EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                ( POTENTIAL).
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           CPOTENTIALS
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                                                                                                                                                                     Local Similarity
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191
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695 AA;
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RESULT 11

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Page 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 IDALCHIPI-PVAKPLSLLOVBIPGTITSWVVIGYSAINSALNPILYTETEPFKE---- 115
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Bulbranden I.T., Bozonyel R., Matthainen T., Sprengel R.;
Piph murine intesisting hormone and foliacie-strumlating hormone
racceptor genes: transcription initiation sites, putative promoter.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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10.487,1993 (Rel. 25, East Sequence update)
10.487,1993 (Rel. 25, East Sequence update)
10.487,1993 (Rel. 24, List Simple Cityon update)
10.487,1993 (Rel. 24, List Simple Cityon update)
10.487,1993 (Rel. 10.487)
10.487,1993 (Les initial phomone receptor)
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Mol. cell. Endocrinol. B8:55-66(1992).
-- FUNCTION: RECEPPOR FOR LOTROPIN-CIORIOGONADOTROPIC HORNONE.
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                               REF.
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Matches 42; Conserv
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                                                                     PONFLIP
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When the Department is intertune of the service of the serv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    *Porcine follicle=criminating hormone receptor.";
*Submitted (SBF-1997) to the EMEN/Genemank/DOBJ databases.
*-I-FONDATION: RECEPTOR ROW FONDATION SUBMITTHE MOSTUVITY
*-OF THIS MECEPTOR IS MEDIATED BY G PROFEINS WHICH ACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLIZIAR LOCATION: Integral membrane protein.
SIMILARIY: BELOMS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSHALSHYSH SUBPAMILY.
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Primar production (1.1...)

Primar production (1.1...)

PRIMARS, PROGUST, GREWERT, 1.

PRIMARS, PROGUST, GREWERT, 1.

PRIMARS, SRONDOLS, PREMENT, 1.

PROSTER, PROGUST, GROWERLENGE, 1.1, 1.

PROSTER, PROGUST, GROWERLENGE, 1.1, 1.

PROSTER, PROGUST, GROWERLENGE, 1.1, 1.

CHOCKELL PROGUST, GROWERLENGE, 1.1, 1.

CHOCKELL PROGUST, TRANSMEMBER, 1.1, 1.

CHOCKEL PROGUST, TRANSMEMBER, 1.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                        MEDITME-96011644; PubMed-7590277;
MEMBY JG., LABAID: MARRASIRI I., 'Ferice M., Bozon V., Couture L., Parlo E., Grebert D., Salesse R.;
This portion follitroph receptor: CORA closing, functional expression and otherwises
                                                                                                                                                                                                                                                                                                                                                     IISSUE-Ovary;
Wang Y. B., Wan S.J., Degen S.J.F.,
Ja Barzer, A.R.,
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EMBL, AP025377; AAC24981.1; -.
HSSP; P23945; 1XUN.
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                    -1- SUBCELGIAR LOCATION: Integral membrane protein.
-1- SMILARITY BENCOMS TO FMILY 1 OF G-PROTEIN COUPLED RECEPTORS. FSB/LSH/TSB SUBFMILY.
-1- SIMILARITY: CORPLAIR 4 leuchne-rich (LRR) repeats.
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Bokaryota, Metazoa, (Chridata, Craniata, Vertebrata, Buteleostomi, Bokaryota, Metazoa, Chordata, Grunognathi, Muridae, Murinae, Rattus. Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

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LSH-R) (Luteinizing hormone receptor).

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protein-coupled receptor family."; Science 245:494-499(1989). STRAIN-EPROGRAGO AND AND ALMERSTRUTE SELLCING.
STRAIN-EPROGRAGO AND AND ALMERSTRUTE SELLCING.
AREASING J. T. PREFILE M. LANKANOOPI J.T. Nejaniemi H.J.;
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Mol. Cell. Endocrinol. 84:127-135(1992)

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MEDILANG-2106631, Publied-2174031,
Thatsi-Meritz C. R., Bencho, E., Reng W., Duffan M.L.;
Thirtoid mature of the ret lutenhinging hormone receptor gene defines
a coluble receptor subspected with hormone binding activity.";
J. Biol., Chem. 265:13365-133861390,
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Local Similarity

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Query Match

MUTAGENESIS

61 TOALCHIPI-FVAKPLSLLOVEIPGTITSWVJGYSAINSALNPILYTLTTRPFKE--- 115

Bernard M.P., Myers R.V., Moyle W.R.; "Cloning of rat lutropin (IH) receptor analogs lacking the soybean

SECUENCE FROM N.A., AND ALTERNATIVE SPLICING MEDLINE-91006819; PubMed-1976554; Cell. Endocrinol, 71:R19-R23(1990). SEQUENCE FROM N.A., AND ALFERNETUR SPLICING.
MEDINE-91126285; Pubmed-2281186; K., Aktolica K., Ascoli M.,
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"Structure of the Intropin/postogenactropin receptor.";
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SBORDEN FROM N.A. SALOMENE R.S. (1 J. F. H.).
NGO Y. J. SLBUDARE R.S. (1 J. F. H.).
STCHORLE Of the luterinizing homone receptor gene and multiple amons of the coding sequence. "I addoctine control of 132-239-2308 (1951).

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                         11 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17 ... 17
                                                                                                                                                                                       ADENYLATE CYCLASE.
SUBCKLULAR LOCATION: Integral membrane protein. Some isoforms may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=B1;
Isoid-P16235-10; Sequence-VSP_001972, VSP_001974, VSP_001979;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOId-P16235-11; Sequence=VSP_001974, VSP_001979;
STAILARTY: BELACORS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
PERITSHYPES SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                   Name=1759;
Isoid=P16235-2; Sequence=VSP_001969, VSP_001977, VSP_001978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=P16235-9; Sequence=VSP_001972, VSP_001977, VSP_001978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSH/LDH/TSH contains 7 leucine-rich (LRR) repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId-P16235-3; Sequence-VSP_001977, VSP 001978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=P16235-5; Sequence=VSP_001971, VSP_001973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isold-P16235-6; Sequence-VSP_001975, VSP_001976;
                                                                                                                                                                                                                                                                                             Event-Alternative splicing; Named isoforms=11;
Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IsoId-P16235-4; Sequence-VSP_001968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=P16235-7; Sequence=VSP_001970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=P16235-8; Sequence=VSP_001972;
                                                                                                                                                                                                                                                                                                                                                                    IsoId-P16235-1; Sequence-Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | March | Marc
MEDLINE-91332007; PubMed-1714448;
                                                                                                                                                                                                                                               he secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dame-1950;
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528 SQUYILSILI-LNVVAFVVICACYIRITFAVQNPELTAP-----NKDTKIAKKMALLIF 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AQIYSVAIFLGINLAAFIIIVFSTGSMFYSVHQSALTATEIRNQVKKEMILAKRFFTVF 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHARTS FREEZE, FEGREROOSE AND FEGRER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LUTROPIN-CHORIOGONADOTROPIC HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.2%; Score 134; DB 1; Length 700; 27.2%; Pred. No. 5.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYTERCELIMIAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL)
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, carb22682.2; JOINED.
9; AAB22682.2; JOINED.
9; AAB22682.2; JOINED.
1; AAB22682.2; JOINED.
AAB22682.2; JOINED.
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InterPro; IPR01611; LRR.
InterPro; IPR001612; LRR_Nterm.
Pfam; PP001001; 7fm_1; 1.
Pfam; PP001001; 7fm_1; 2.
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HSSP; P22888; 1LUT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               779 TDPLCMAPILPPAISASLKVPLLTVSKAKILLVLFTPINSCAMPFLTAIFTKNFRKDFFV 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AQIYSVAIPLGINGAAFIIIVFSYGSMFYSVHQSAITAIEIRNQVKKEMILAKRFFFIVF
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROGETE; PRODUZTY, G_PROPER, RECEP_FL_1; 1.

PROSITE; PSODOZY, G_PROPER, RECEP_FL_2; 1.

G-proteid, coupled receptor; Transmembrane; Glycoprotein; Stignal;
PROSPIDE; Repeat; Leucine-fich repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 692;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tudels
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EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4B57229180563A44 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 IMSKEGCIEVQAQIYKTETSSITHNEHSRKNPCSSAPR 676
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 132.5; DB 26.6%; Pred. No. 8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRR 2.
LRR 3.
LRR 4.
LRR 5.
ERR 6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR000376; GPCR_Rhodpsn.
InterPro; IPR001611; LRR.
InterPro; IRR000372; LRR_Nterm.
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Functional annotation of a full-length mouse CDNA collection.";
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Huhtaniemi I.T., Eskola V., Pakarinen P., Matikainen T.,
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